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MT1A_SHEEP
MT1C_SHEEP
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130 AA; 13913 MW; FD58E2D3C99D1644 CRC64;

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                                        ALIATORNIANU, PRI; 130 AA.
P62931; P06687; Q40999; Q70313; O9M3X4;
01-JAN-1988 (Rel. 06, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 F precursor (Pal F) (Feaalbo05/Feaalbo11) [Contains: Albumin 1 F chain b (Palb F) (Leginsulin F); Albumin 1 F chain a (Pale F) [
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12755688;
Gressent F., Rahioui I., Rahbe Y.;
"Characterization of a high-affinity binding site for the pea albumin
lb entomotoxin in the weevil Sitophilus.";
Eur. J. Blochem. 270:2429-2435(2003).
-!- FUNCTION: PAlb binds to basic 7S globulin (BG) and stimulates its
posphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide (By similarity). Toxic to various insects through binding
to a high affinity binding site in the insect gut.
-!- PTM: The C-terminal glycine may be removed from PAlb.
-!- PTM: PAlb displays a cysteine-Knot (knottin) fold.
                                                                                                                                                                                                                     STRAIN=CV. Frieson, TISSUE-Seed, Louis S., Delobel B., Gressent F., Rahioui I., Quillien L., Vallier A., Rahbe Y., "Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "PAlb, an insecticidal protein extracted from pea seeds (Pisum sativum): 1H-2-D NMR study and molecular modeling.";
                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14556622; DOI=10.1021/bi0348031;
Jouvensal L., Quillien L., Ferrasson E., Rabbe Y., Gueguen J.,
Vovelle F.;
                                                                                                                                                                                                                                                                                                                                 Delobel B., Grenier A., Gueguen J., Ferrasson E., Mbailao M., "Use of a polypeptide derived from a PAlb legume albumen as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AJ574793; CAE00465.1; -.
PDB; 1P8B; NMR; A=27-63.
InterPro; IPR011036; PH related.
Db.Structure; Direct protein sequencing; Plant toxin; Seed storage protein; Signal.
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Albumin 1 F chain a.
Potential.
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                                     130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         Patent number WO9958695, 07-MAY-1999.
                                    PRT;
                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 27-63, AND FUNCTION.
                                                                                                                                                                                                                                                                                           Plant Sci. 167:705-714(2004).
                                                                                                                                                                                                                                                                            from four legume species
                                   STANDARD;
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SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.

STRAIN-CV. Greenfeast; TISSUE-Seed;

MEDLINE-86278210; PubMed=1755437;

Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,

Radiover R.J., Kortt A.A., Inglis A.S.;

"Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds.";

"Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds.";

"Gene structure, protein in seeds.";

"Gene structure, protein in pea seeds.";

"Gene structure, protein in seeds.";

"Gene structure, protein in the insect gut (By similarity).

"TISSUE SPECIFICITY: Major comopnent of both the cotyledons and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DEVELOPMENTAL STAGE: Increasing expression during seed development followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                     ALIA PEA STANDARD; PRT; 130 AA.
P62926; P08687; Q40999; Q9M3X4;
O1-JAN-1988 (Rel. 06, Created)
O1-JAN-1988 (Rel. 06, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 A precursor (PA1 A) [Contains: Albumin 1 A chain b (PA1b A) [Leginsulin A); Albumin 1 A chain a (PA1a A)].
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatobhyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
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100.0%; Score 217; DB 1; Length 130; 100.0%; Pred. No. 1.5e-17; .ive. 0; Mismatches 0; Indels
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                                                                                                                                                      ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 63
                                                                                                                       1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
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Pred. No. 2e-17;
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Plant toxin; Seed storage protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
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48 By
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13912 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisum sativum (Garden pea).
                              Local Similarity 100.
1es 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.33
Matches 36; Conservative
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1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37

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Mismatches

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36; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     PRT; 130 AA.
P62929; P08667; Q40999; Q7XTK6; Q9M3X4;
01-JAN-1988 (Rel. 06, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 D precureor (PAI D) (PsaAlbot2) [Contains: Albumin 1 D chain b (Raingulin D); Albumin 1 D chain activum (Garden pea).
Bigum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                               embryonic axes of mature seeds.
DEVELOPMENTAL STAGE: Increasing expression during seed development
followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        germination.

PTM: The Cterminal glycine may be removed from PAlb.

MISCELLANBOUS: The protein sequenced in Ref.2 was probably a mixture of the products of genes C and D, PAlb being of C origin while PAla is of D origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ing, Plant toxin; Seed storage protein; Signal.
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                        STRAIN=CV. Frisson, TISSUE-Seed;
bouls S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rahbe Y.;
"Molecular and biological screening for insect-toxic seed albumins"
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 70-122, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 130;
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By similarity.
By similarity.
823AA340ACD9535C CRC64;
ASCNGVCSPFEMPPCGTSACRCIPVGLVVGYCRNPSG 63
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Albumin 1 D chain b.
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                                                                                                                                                                                                                                                                                                              TISSUE=Seed;
MEDLINE=86278210; PubMed=3755437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR011036; PH related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 B
13916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ574794; CAE00466.1; -.
                                                                                                                                                                                                                                                                  from four legume species.";
Plant Sci. 167:705-714(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.78;
97.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequenci
SIGNAL 1
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=3888;
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DISULFID
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CHAIN
PROPEP
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Score 212; DB 1; Pred. No. 5.7e-17;

Best Local Similarity

Query Match

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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                              P62930; P08687; Q40999; Q7XZC1; Q9M3X4; 01-JAN-1988 (Rel. 06, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Albumin 1 B precursor (PA1 B) (P8aAlb014) (P8a) [Contains: Albumin 1 E chain a (PA1a B)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. Frisson, TISSUE-Seed;
Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Valler A., Rabbe V.;
Waller A., Rabbe V.;
"Molecular and biological screening for insect-toxic seed albumins
from four legume species.";
Plant Sci. 167-705-714(2004).
-!- FUNCTION: PALD binds to basic 7S globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide. Toxic to various insects through binding to a high
affinity binding site in the insect gut (By similarity).
-!- PTM: The C-terminal glycine may be removed from PAlb.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantãe; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum. NCBI_TaxID=3888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morton R.L., Ellery A.J., Higgins T.J.;
"Downstream elements from the pea albumin 1 gene confer sulfur responsivenes on a reporter gene.";
Mol. Gen. Genet. 259:309-316(1998).
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1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                          ASCNGVCSPFEMPPCGTSACRCIPVGLFIGYCRNPSG 63
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Albumin 1 E chain a Potential.
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By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Sor send an email to license@isb-sib.ch).
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ574795; CAE00467.1; -
InterPro; IPR011036; PH_related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13778 MW;
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                                                                                                                                                                                                                                                                                                                                                       Pisum sativum (Garden pea).
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                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=CV. Greenfeast;
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63
69
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9749674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO. Birte; TISSUE-Cotyledon;

A Domoney C. Elils N., Welham T.;

Bonneney C., Elils N., Welham T.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

I. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ atabases.

POSPORTION: PAID binds to basic 78 globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide. Toxicus insects through binding to a high affinity binding site in the insect gut (By similarity).

C -- TISSUE SPECIFICITY: Major comopnent of both the cotyledons and embryonic axes of mature seeds.

C -- DBVELOPMENTAL STAGE: Increasing expression during seed development followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                 STRAIN=CV. Greenfeast; TISSUB=Seed;
MEDLINE=86278210; PubMed=3755437;
Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Higgins T.J.V., Kort A.A., Inglis A.S.;
Blagrove R.J., Kort A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
                       Fig. STANDARD; PRT; 130 AA.

P62927; P08687; Q40999; Q9M3X4;
01-3AN-1988 [Rel. 06, Created)
25-OCT-2004 [Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
Albumin 1 B precursor [PA] B) [Contains: Albumin 1 B chain b (PAlb B) sum sativum (Garden pea).

Pisum sativum (Garden pea).

Pisum sativum (Marden pea).

Pisum sativum (Marden pea).

Pisum sativum (Marden pea).

Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY
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Potential.
Albumin 1 B chain a.
Albumin 1 B chain a.
Potential.
By similarity.
By similarity.
M -> I (in Ref. 2).
Q -> P (in Ref. 2).
W, F8B134A334490F5F CRC64;
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PTM: The C-terminal glycine may be removed from PAlb
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InterPro; IPR011036; PH_related
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10 M
120 Q
13970 MW;
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DISULFID
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CONFLICT
SEQUENCE
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                 RESULT 5
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SEQUENCE FROM N.A.
NCBI_TaxID=3888;
                                                                                                              Length 130;
                                                                                                            95.4%; Score 207; DB 1; Luilarity 91.9%; Pred. No. 2.2e-16; Conservative 3; Mismatches 0;
                                                                                                                                Local Similarity
les 34; Conserv
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Gaps

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Indels

27 ASCNGVCSPFEMPPCGSSACRCIPVGLVVGYCRHPSG 63

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PRT; 130 AA.

PG5928; P08687; Q40999; Q7XZC0; Q9M3X4;
01-JAN-1988 (Rel. 96, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
Albumin 1 C precursor (PAL) (C) (PsaAlbols) (Contains: Albumin 1 C chain b (PAL) C) (Leginsulin C); Albumin 1 C chain a (PAL) C)
Pisum activum (Garden pea).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.,
"Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
activities and occurence of seed albumin 1b toxins.";
submitted (JUD-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784951; CAH05251.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Vicia. NCBI_TaxID=3910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. Frisson; TISSUE=Seed; Louis S., Delobel B., Gressent F., Rahioui I., Quillien L., Vallier A., Rabbe Y.; "Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 27-63, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; reurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD8EF1B021A73DD7 CRC64;
                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  putative albumin 1b. putative albumin 1a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 194; DB 2;
Pred. No. 5.4e-15;
2; Mismatches 3;
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                                                             Created)
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63
>96
96
10546 MW; 1
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Plant Sci. 167:705-714(2004).
                                                                                                           Putative albumin 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.4%;
Best Local Similarity 86.5%;
Matches 32; Conservative
                                                             (TrEMBLrel. 28,
                             PRELIMINARY;
                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA;
                                                                25-OCT-2004
                                                                                            25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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SIGNAL
                                Q6A1C7
Q6A1C7;
RESULT 6
Q6A1C7
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Best Loca Matches

1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37

insecticidal

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Gaps

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61

Length 98 Indels

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rahbe Y.;
"Molecular and biological screening for insect-toxic seed albumins
from four legume species.";
Plant Sci. 167:705-714 (2004).
EMBL; AJS74791; CAE00463.1; -.
ESQUENCE FROM N.A.

EDUSTICE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O., Chessel D., Rahbe Y.;

Chessel D., Rahbe Y.;

"Broad screening of the legume family for variability of insectici "Broad screening of the legume family for variability of insectici "Broad screening of the legume family for variability of insectici "Broad screening of seed albumin and proxime.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O92QXO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 precursor (Al) [Contains: Albumin 1 chain b (Alb)
(Leginsulin); Albumin 1 chain a (Ala)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 159; DB 2; Length 10
Pred. No. 6.3e-11;
6; Mismatches 7; Indels
                                                                                                       activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784944; CAH05244.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA; 10982 MW; 281D9CE0F8E83611 CRC64;
                                                                                                                                                                                      1 27 Potential.

28 62 putative albumin 1b.

71 >98 putative albumin 1a.

98 98 AA; 10484 MW; B28B2E3919403D53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                        Score 155,
Pred. No. 6.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                                                                                                                                                                                                                                                                                                                                                                                                          2 SCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 ACSGGCSPFEMPPCGSSDCRCIPWGLVAGYCINPT
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Ala, albumin la.
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                                                                                                                                                                                                                                                                                                                      73.3%; Score 159; 74.3%; Pred. No. 6
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nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                26;
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ALB1_GLYSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                 Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds."

J. Biol. Chem. 261:11124-11130(1986)

-! PUNCTION: PAID binds to basic 78 globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide. Toxic to various insects through binding to a high affinity binding site in the insect gut (By similarity).

-! TISSUE SPECIFICITY: Major component of both the cotyledons and embryonic axes of mature seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                              development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR011036; PH related.
Direct protein sequencing; Plant toxin; Seed storage protein; Signal.
SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                        PIM: The C-terminal glycine may be removed from PAlb. MISCELLANBOUS: The protest sequenced in Ref.2 was probably a mixture of the products of genes C and D, PAlb being of C origin while PAla is of Dorigin.
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                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: Increasing expression during seed develor followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> H (in Ref. 2).
12C8EA2B8300A723 CRC64;
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Last annotation update)
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Potential.
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Canavalia brasiliensis (Brazilian jack bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
By similarity.
By similarity.
N -> H (in Ref.
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  MEDLINE=86278210; PubMed=3755437
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nes 28; Conserv
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                                                                                                                                                                                                                                                                                                                        germination.
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Best Local &
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Length 100;

06A1D4;

RESULT 8
96A1D4
AC 96A1
DT 25-0
DT 25-0
DT 25-0
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Similarity
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SEQUENCE
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Best Local
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SIGNAL
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                      Matches
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                                                                                                              SEQUENCE FROM N.A.

Tan J.Z., Lou C.F., Hirano H.;

Manalysis (19,01 cl.), Hirano H.;

Wild species (19,01 cl.), Hirano H.;

Chin. J. Appl. Environ. Biol. 5:259-263(1999).

-!- FUNCTION: Alb binds to basic 75 globulin (BG) and stimulates its phosphorylation activity (By similarity).

-!- FUNCTION: Alb pinds to pay similarity).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Louis S., Delobel B., Gressent F., Rahioui I., Quillien L., Vallier A., Rahbe Y., "Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albumin 1 chain b (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albumin 1 chain a (Potential)
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15426 MW; 519D9CEAB8924855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . similarity.
EE5457D8D09070CC CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 159; DB 1;
Pred. No. 7.3e-11;
8; Mismatches 6;
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By similarity.
By similarity.
By similarity.
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Plant toxin; Seed storage protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AJ011935; CAA09880.2; -.
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51 By
12963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Sci. 167:705-714(2004).
EMBL, AJ574789; CAE00461.1; --
HSSP; Q39837; 1JU8.
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(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
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les 23; Conservative
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57
118
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26
34
119 AA;
                                                                     NCBI_TaxID=3848;
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01-OCT-2003
01-OCT-2003
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DB 2;

Score 156;

71.98;

Query Match

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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                      Astragalus monspessulanus.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids 1; Fabales, Fabaceae, Papilionoideae, Galegeae, Astragalus.
NCBI_TAXID=287756,
 Gaps
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MEDLINE-54357216; PubMed-8076638;
Watanabe Y., Barbashov S.F., Komatsu S., Hemmings A.M., Miyagi M.,
Tsunasawa S., Hirano H.;
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Q19837; 049854;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
(Leginsulin); Albumin 1 Contains: Albumin 1 chain b (Alb)
(Leginsulin); Albumin 1 chain a (Ala)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
 Indels
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                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 155; DB 2; Le
68.6%; Pred. No. 1.8e-10;
wismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       putative albumin 1b. putative albumin 1a.
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                                                      30 CSGACSPFEMPPCRSSDCRCIPIGLVAGYCTYPS
                                                                                                                                                     100 AA
                                   3 CNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS
   3; Mismatches
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                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
   25; Conservative
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64
>100
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SEQUENCE FROM N.A.
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b (A1b)

us-09-674-496d-6.rup

Hirano

AND

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                   Phaseolus angularis (Adzuki bean) (Vigna angularis).

Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.

NCBL_TaxID=3914;
                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 270:1269-1276(2003).
-!- FUNCTION: Alb binds to basic 75 globulin (BG) and stimulates its
phosphorylation activity (By similarity).
-!- PIM: The C-terminal glycine may be removed from Alb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,
Nishiuchi Y., Hirano H.;
                                                                                                                                                                                                                           Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,
Nishiuchi Y., Hirano H.;
                                                                                                                                                                                                                                                       "A possible physiological function and the tertiary structure of a kDa peptide in legumes "; Eur. J. Biochem. 270:1269-1276(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, roside eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Vigna. NCBI_TaxID=3916,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albumin 1 chain b (By similarity).
Potential.
Albumin 1 chain a (Potential).
By similarity.
By similarity.
By similarity.
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Albornin 1 precureor (Al) [Contains: Albumin 1 chain b (Alb) (Leginsulin); Albumin 1 chain a (Ala)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070A562F346FBB61 CRC64;
Albumin 1 precursor (A1) [Contains: Albumin 1 chain (Leginsulin); Albumin 1 chain a (A1a)] (Fragment).
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Pred. No. 2.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant toxin; Seed storage protein; Signal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (6 or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
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PubMed=12631285;
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PubMed=12631285;
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es 25; Conserv
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q39837; 1JU8
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SEQUENCE FROM N.A.
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Q9FRT8;
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NON TER
SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                 PubMed=12631285;
Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,
Nishiuchi Y., Hirano H.;
Nishiuchi Y., Hirano H.;
Alpossible physiological function and the tertiary structure of a 4-kDa peptide in legumes.";
Rur. J. Biochem. 270:1269-1276(2003).
-I- FUNCTION: Alb binds to basic 78 globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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   plant insulin-
cDNA cloning.";
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                                                                                       STRAIN=cv. Miyagishirome;
Tan J.Z., Lou C.F., Hirano H.;
"Analysis of leginsulin gene in soybean cultivar (Glycine max)
wild species (Glycine soja) ";
Chin. J. Appl. Environ. Biol. 5:259-263(1999).
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Albumin 1 chain a (Potential)
Potential.
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Pred. No. 2.8e-10;
8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: The C-terminal glycine may be removed from Alb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-structure, Plant toxin, Seed storage protein, Signal
 "A peptide that stimulates phosphorylation of the binding protein. Isolation, primary structure and Eur. J. Biochem. 224:167-172(1994).
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V->A: Decreased P->A: Decreased b
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EMBL, AJ223037, CAA11040.1; -
PIR, S48192, S48192.
PDB, 1JU09, NMR, A=20-56.
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59.5%;
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                                                                                                                                                                                                                                 STRAIN=cv. Miyagishirome;
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(Rel. 40,
(Rel. 45,
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tes 22; Conserv
                                                                           SEQUENCE FROM N.A
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117
22
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34
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Q9FRT9;
16-OCT-2001
16-OCT-2001
25-OCT-2004
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MUTAGEN
SEQUENCE
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CHAIN PROPEP

RESULT 14
ALB1\_PHAAN

44446

Matches

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SIGNAL PROPEP

CHAIN

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Gaps

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7; Indels

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89

DB 1; Length 90;

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Query Match
Best Local Similarity 65.7
Matches 23; Conservative
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Best Local Similarity
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28
72
99
89 AA;
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NON TER
SEQUENCE
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Q6A1C8;
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                     Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds."; "J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryotta. Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Hedysareae; Onobrychis.
VCBI_TaxID=3882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Broad screening of the legume family for variability of insecticidal activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ78459; AAD652491, -1, -.
           peptide in legumes.";
J. Biochem. 270:1269-1276(2003).
FUNCTION: Alb binds to basic 78 globulin (BG) and stimulates its phosphorylation activity (By similarity).
PTM: The C-terminal glycine may be removed from Alb.
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;
 possible physiological function and the tertiary structure of
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                        Potential.
Albumin 1 chain b (By similarity)
Potential.
Albumin 1 chain a (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                   Length 89;
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Last annotation update)
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putative albumin 1b.
putative albumin 1a.
                                                                                                                                                                                                                                                                                                                 Score 153; DB 1;
Pred. No. 2.9e-10;
5; Mismatches 8;
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                                                                                                                                                                                                                                                                         similarity
                                                                                                                                                                        HSSP; 039837; 1JU8.
Plant toxin; Seed storage protein; Signal.
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598
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10830 MW;
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9711 MW;
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98 AA;
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Local Sim
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
euroaids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trigonella.
NCBI_TaxID=78534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Liouis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;
"Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784950; CAH05250.1;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Millettieae, Mundulea
                                                 Gaps
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  Length 98;
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Score 153; DB 2; L. Pred. No. 3.1e-10; 7; Mismatches 5;
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Pred. No. 9e-10;
4; Mismatches
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                                               7; Mismatches
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25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
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64
99
10783 MW;
  70.5%;
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l Similarity 72.7%;
24; Conservative
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Query Match
Best Local Simi
Matches 26;
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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
Blagrove R.J., Fortt A.B., and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Blol. Chem. 261:11124-11130(1986).
"Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds."; J. Biol. Chem. 261:11124-11130(1986).
                                                                                        SEQUENCE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,

Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,

Chessel D., Rahbe Y.;

"Broad screening of the legume family for variability of insecticidal
sctivities and occurence of seed albumin 1b toxins.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ784947; CAH05247.1; -.
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.,
"Broad ecreening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ784945; CAHOS245.1;
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Bukaryota, Vizidiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Millettieae;
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25 64 putative albumin 1b.
71 >101 putative albumin 1a.
101 101 MW; 26ECD6B970BD10E2 CRC64;
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(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                Potential.
putative albumin 1b.
putative albumin 1a.
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putative albumin 1b.
putative albumin 1a.
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70.0%; Pred. No. 1.8e-09;
iive 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                            68.4%; Score 148.5; DB 74.4%; Pred. No. 1e-09; ive 2; Mismatches
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Best Local Similarity 74.4%;
Matches 29; Conservative :
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hes 28; Conserv
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6A1D3
Q6A1D3;
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SIGNAL
                                                                                                                                                                                                                                                               Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                             CHAIN
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106A103
10 AC Q6A103
DT 25-OC DT 25-OC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                          phaseclus vulgaris (Kidney bean) (French bean).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotylache eudicots; rosida;
Spermatophyta; Magnoliophyta; eudicotylache; phaseolache eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolus
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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.,
"Gene structure, protein structure, and regulation of the synthesis of sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Psoraleeae,
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Gressent F., Rahioui I., Quillien L., Vallier A., Palbel B., Gressent F., Rahioui I., Quillier A., Rahbe Y., Wallier A., Rahbe Y., "Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11923 MW; E420417E90D351AE CRC64;
                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%; Score 143.5; DB 2;
larity 72.2%; Pred. No. 4.2e-09;
Conservative 1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
putative albumin 1b.
putative albumin 1a.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Alb, albumin 1b. Ala, albumin 1a.
109 AA.
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 PRT;
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                                                                                           Albumin 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                from four legume species.";
Plant Sci. 167:705-714(2004).
EMBL, AJ514792; CAE00464.1; --
HSSP; Q39837; lJUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
 PRELIMINARY;
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65
×109
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62
99
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74 >1
109 1
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                                                                                                                                                                                                   NCBI_TaxID=3885;
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SIGNAL
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8

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SEQUENCE FROM N.A.
Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seed8.";
J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rabbe Y.,

"Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins ";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ784946; CAH05246.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula (Barrel medic).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Louis S., Delobel B., Gressent F., Rahioui I., Quillien L., Vallier A., Raheb Y., Wholecular and biological screening for insect-toxic seed albumins
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15727 MW; F35A1A5A9EDA9E2F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
putative albumin 1b.
putative albumin 1a.
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Last sequence update)
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64.7%; Pred. No. 1.9e-07;
cive 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 60.8%; Score 132; DB 2; Local Similarity 64.7%; Pred. No. 8.3e-08; es 22; Conservative 6; Mismatches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSGICSPFEMPPCPSSCRCIPVILIGGNYVDPS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 CSGICSSFEMPPCRSSSCRCIPVVLLGGNCVDPS 62
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63
598
98
98
10691 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from four legume species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA;
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25-OCT-2004 (
25-OCT-2004 (
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SEQUENCE
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Q6A1D0
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rabbe Y.;
"Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784942; CAH05242.1;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae, Papilionoideae, Trifolieae, Melilotus. NCBI_TaxID=47082;
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Desmodieae,
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Pred. No. 4.6e-08;
7; Mismatches 9; Indels
                                                                                                     Score 138; DB 2; Length 99;
Pred. No. 1.7e-08;
B; Mismatches 8; Indels
                                                 10767 MW; 27ACD82ABC4B2B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB9B9278F3EF5B06 CRC64;
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Last sequence update)
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putative albumin 1b.
putative albumin 1a.
                                                                                                                                                                                                                                                            27 ACSGACFPFQMPPCGSTDCRCVPWGLFVGQCIDPIG 62
                                                                                                                                                                                                                          2 SCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AA
                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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19 55
64 >91
91 91
91 AA; 9890 MW;
                                                                                                        63.6%;
55.6%;
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                                                                                                                                                                20; Conservative
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                                                 99 AA;
                                                                                                                                       Local Similarity
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NCBI_TaxID=287750;
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DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

By Utative albumin I precursor (Fragment).

So Mundulas sericea.

OC Bukarycta; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

CC Eukarycta; Viridiplantee; Papalionoideae; Millettieae; Mundulea.

CN CDI Traches; FROM N.A.

RA Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,

RA "Gene structure, protein in pea seeds.";

CA SEQUENCE FROM N.A.

RA CHOIS S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,

RA Chessel D., Rahbe Y.;

CHOSEL D., Rabbe Y.;

RA Chessel D., Rahbe Y.;

CHOSEL A. A. A. CHOSE S. CHOLOS A CHARLOS A CHOLOS A CHOLOS A CHARLOS A CHARLO
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Search completed: March 28, 2005, 09:00:06 Job time : 87 secs

3 CNG--VCSPFEMPPCG-TSACRCIPVGLVIGYCRNPS 36

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C, Accession: A55677
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C, Date: 16-bug-1988 #text_change 09-Jul-2004

C, Date: 16-bug-1988 #text_change 09-Jul-2004

C, Date: 16-bug-1988 #text_change 09-Jul-2004

C, Accession: A25014

A, Title: Gene Structure, protein structure, and regulation of the synthesis of a sulfur-Axeference number: A25014; MUID:86278210; PMID:3755437

A, Accession: A25014

A, Molecule type: DNA

A, Residues: 1-130 <HID: A15014

A, Residues: 1-14014

A, Residues: 1-14014

A, Residu
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19130
R;Smye, R.
submitted to the EMBL Data Library, November 1996
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A,Molecule type: protein
A,Residues: 20-30,'M',32-39 <BAR>
F;1-19/Domain: propeptide #status predicted <PRO>
F;2-0-56/Product: insulin-like growth factor S11 #status experimental <MAT>
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Pred. No. 1.4e-10;
8; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 17/1
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-130/Product: albumin #status predicted <MAT>
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Pred. No. 1.6e-17;
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Local Similarity 97.3%;
les 36; Conservative
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L Similarity 59.5%;
22; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1642 <WIL>
A;Cross-references: UNIPROT:062055; EMBL:281465; PIDN:CAB03861.1; GSPDB:GN00020; CESP:CO:
C;Genetics:
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R;Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.
J. Exp. Med. 180, 1763-1774, 1994
A;Pitle: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the c nand functions as a transcriptional repressor.
A;Reference number: 138869; MUID:95053707; PMID:7964459
A;Accession: 138869; MUID:95053707; PMID:7964459
A;Accession: 138869
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1104 «RES>
A;Accession: RING finger homology «RRN>
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A;Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca. A;Reference number: A55677; MUID:95213013; PMID:7698745
A;Accession: A55677
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A/Map posttion: 3p21.3-3p21.2
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F;1-32/Domain: signal sequence #status predicted <SIG>F;1-37/Porduct: laminin beta-2 chain #status predicted <MAT>F;283-374/Domain: laminin-type EGF-like homology <LE01>F;347-407/Domain: laminin-type EGF-like homology <LE02>
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C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                               A;Gene: CESP:CO9F9.2
A;Map position: 2
A;Introns: 75/3; 103/2; 220/1; 552/1; 1500/3; 1517/1; 1578/3
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Matches 15; Conservative
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A;Cross-references: GB:X79683
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metallothionein Ic - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: 800810
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel
A;Reference number: 800808; MUID:88254812; PMID:3383853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-61 <PET>
A;Cross-references: UNIPROT:P09577; EMBL:X07973; NID:g1338; PIDN:CAA30785.1; PID:g1339
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S00808, Hannan, F:; Mercer, J.F.B.
Bur. J. Blochem. 174, 417-424, 1988
A;Title: The sheep metallothionein gene family. Structure, sequence and evol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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    Bur. J. Biochem. 160, 579-585, 1986
A;Title: Structure and regulation of the sheep metallothionein-Ia gene.
A;Reference number: 146414; MUID:87053978; PMID:3780723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X00953; NID:g1825; PIDN:CAA25464.1; PID:g1826
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                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-49, '6',51-61 <PET2>
A;Cross-references: EMBL:XO4626; NID:g4218467
B;Peterson, M.G.; Lazdins, I.; Danks, D.M.; Mercer, J.F.
Biochem. 143, 507-511, 1984
A;Title: Cloning and sequencing of a sheep metallothionein CDNA.
A;Reference number: 146559; MUID:85003624; PMID:6434305
A;Accession: 146559
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Pred. No. 3.3;
0; Mismatches 1:
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Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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Local Similarity 44.4%;
les 12; Conservative (
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C;Superfamily: metallothionein
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C;Superfamily: metallothionein
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Matches 12; Conservative
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A, Residues: 1-61 < PET>
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A; Residues: 1-61 <PET>
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C;Species: Ovis oxientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis oxientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis oxientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S00808; 146414; 146559
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Bur. J. Blochem. 174, 417-424, 1988
A;Accession: S00808
M;MID:88254812; PMID:338383
A;Accession: S00808
A;Residues: 1-61 <PFT1>
A;Residues: 1-61 <PFT1>
A;Cross-references: UNIPROT:P04356; GB:X04626; NID:g4218467; PIDN:CAA28299.1; PID:g42184
R;Peterson, M.G.; Mercer, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-61 < wins.
A; Cross-references: UNIPROT: P04356
A; Cross-references: UNIPROT: P04356
A; Cross-references: UNIPROT: P04356
A; Cross-references: UNIPROT: P04356
A; Cross-references: Calf liver
A; Note: 49-Ile was also found
C; Comment: The vertebrate metallothioneins contain two metal-binding domains. Clusters c
C; Comment: Cysteine clusters can also chelate univalent metal ions. As many as 18 differ
C; Superfamily: metallothionein
C; Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
E; 1-29/Domain: beta < NNI2>
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F;1/Modified site: acetylated amino end (Met) #status experimental
F;5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F;5,7,13,15,19,141,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A03279
R;Winge, D.R.; Gray, W.R.; Zelazowski, A.; Garvey, J.S.
Arch: Biochem: Biophys. 245, 254-262, 1986
A;Fitle: Sequence and antigenicity of calf metallothionein II.
A;Reference number: A03279; MUID:86129456; PMID:3947100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                           #status atypical <LE05>
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7
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44.4%; Pred. No. 3.3;
iive 0; Mismatches 13; Indels
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F,410-467/Domain: laminin-type EGF-like homology <LEG3>
F,470-519/Domain: laminin-type EGF-like homology <LEG4>
F,522-522-522/Domain: laminin-type EGF-like homology #status & F,783-828/Domain: laminin-type EGF-like homology <LEG6>
F,831-874/Domain: laminin-type EGF-like homology <LEG6>
F,877-924/Domain: laminin-type EGF-like homology <LEG9>
F,877-924/Domain: laminin-type EGF-like homology <LEG9>
F,985-1034/Domain: laminin-type EGF-like homology <LEG9>
F,985-1034/Domain: laminin-type EGF-like homology <LEG1>
F,1037-1091/Domain: lamin
                                                                                                                                                                                                                                                                                                                                                                                                        F;1142-1186/Domain: laminin-type EGF-like homology <LE13>
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4; Mismatches
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nes 12; Conservative
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Matches
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Gaps

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3; Indels

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testis-specific protein (clone mst(3)gl-9) - fruit fly (Drosophila melanogaster)
testis-species: Drosophila melanogaster
c;Species: Drosophila melanogaster
c;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00340
R;Kuhn, R; Schaefer, M.
R;Kuhn, R; Schaefer, M.
R;Kuhn, R; A: 7, 4454, 1988
R;File: Cis-acting regions sufficient for spermatocyte-specific transcriptional and spen A;Reference number: S00340; MUID: 88211557; PMID: 2835228
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A;Title: (Cu,Zn)-metallothioneins from fetal bovine liver. Chemical and spectroscopic prof. A;Reference number: A92490; MUID:85261416; PMID:4019500
A;Accession: A23889
Riptorian Bolsvenue, R.J.; Cox, G.N.
Riptorian Bolsvenue, R.J.; Cox, G.N.
Mol. Biochem. Parasitol. 56, 39-48, 1992
Mol. Biochem. Parasitol. 56, 39-48, 1992
A;Title: Isolation of putative cysteine protease genes of Ostertagia ostertagi.
A;Reference number: A48454; MUID:93116804; PMID:1475000
A;Accession: B48454
A;Status: preliminary
A;Accession: B48454
A;Status: preliminary
A;Residues: 1-174 < PRA-
A;Residues: 1-174 < PRA-
A;Residues: UNIPROT:Q06544; GB:M88505; NID:g159951; PIDN:AAA29436.1; PID:g159952
A;Cross-references: UNIPROT:Q06544; GB:M88505; NID:g159951; PIDN:AAA29436.1; PID:g159952
A;Accessionerimental source: larva
A;Note: sequence extracted from NCBI backbone (NCBIN:121411, NCBIP:124017)
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase; protein degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: P08175; EMBL: Y00831; NID: 98650; PIDN: CAA68761.1; PID: 98651
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C,Species: Bos primigenius taurus (cattle)
C,Date: 07-Mar_1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 2;
Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccepccepccepccepccepcceccepcycpN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 2; Pred. No. 16; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 1
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: FlyBase:FBgn0002862
C,Superfamily: fruit fly testis-specific protein
C,Keywords: sex-specific protein; testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 25.8%; Score 56; DB Local Similarity 38.2%; Pred. No. 8.7; Pred 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1.61 × VMUN-
A;Cross-references: UNIPROT: P58280
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.8%;
Best Local Similarity 44.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S GVCSPFEMPPCG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 GCCRPYEFPPCG 31
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A; Residues: 1-56 < KUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: FlyBase:Mst87F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S00340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: 803539
A; Molecule trype: mRNA
A; Accession: 803539; MolDisylpty, Fig. 20250; PIDN: CAA34561.1; PID: 957251
A; Accession: 803539
A; Molecule trype: mRNA
A; Residues: 1-1801 «HUNA
A; Crogs-references: UNIPROT: P15800; EMBL: X16563; NID: 957250; PIDN: CAA34561.1; PID: 957251
C; Complex: Laminins are trimers of an alpha-type abenert membrane proteins to promote C; Function:
A; Description: interact with cells and with other basement membrane proteins to promote C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C; Reywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
C; Superfamily: laminin beta-2 chain #status predicted <NAT>
F; 268-134/Domain: signal sequence #status predicted <NAT>
F; 268-134/Domain: alminin-type EGF-like homology <LEGO>
F; 268-134/Domain: laminin-type EGF-like homology <LEGO>
F; 269-1038/Domain: laminin-type EGF-like homology <LEGO>
F; 1041-1095/Domain: laminin-type EGF-like homology <LEGO>
F; 1041-1045/Domain: laminin-type EGF-like homology <LEGO>
F; 1041-104
                                                                                                                                                                                                                                                                                                                                                                                                             MWRTS

laminin beta-2 chain precursor - rat

laminin beta-2 chain precursor - rat

laminin beta-2 chain precursor - rat

laminin beta-2 chain chain B3; S-laminin

lyspecies: Rattus norvegicus (Norway rat)

C;pecies: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004

C;Accession: S03539

C;Accession: S03539

R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.

Nature 338, 229-234, 1989

A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurch synaptic number: S03539; MUID:89159410; PMID:2922051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1.
F;145-50/Disulfide bonds: #status predicted
F;455-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status }
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
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                                                                                                                                        Gaps
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                                                              Length 61;
                                                                                                                                        13; Indels
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                                                                     DB 2;
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                                                                                                   Pred. No. 3.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58;
Pred. No.
                                                                         Score 60;
Pred. No. 3
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                                                                                                                                                                                                             SCNG--VCSPFEMPPCGTSACRCIPVG 26
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nilarity 41.7%;
Conservative 2
                                                                  Query Match
Best Local Similarity 44.4%;
Matches 12; Conservative
C; Superfamily: metallothionein
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Best Local Similarity
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0; Mismatches

cathepsin B-like cysteine proteinase (EC 3.4...-) CP-3 - nematode (Ostertagia ostertagi)

C;Species: Ostertagia ostertagi C;Date: 01-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

Length 61;

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A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-813 - WIL-
A;Rosidues: 1-813 - WIL-
A;Cross-references: UNIRROT:019673; EMBL:Z71261; PIDN:CAA95805.1; GSPDB:GN00019; CESP:F2
A;Experimental source: clone F21C3
                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-452 <RES>
A;Cross-references: UNIPROT:Q13685; GB:M95627; NID:g870802; PIDN:AAA68889.1; PID:g870803
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C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Duguid, J.R.; Rohwer, R.G.; Seed, B.
Proc. Natl. Acad. Sci. U.S.A. 85, 5738-5742, 1988
A;Title: Isolation of cDNAs of scrapie-modulated RNAs by subtractive hybridization of a A;Reference number: 148171; MUID:88289792; PMID:2456582
,Title: Identification of a new immunoglobulin superfamily protein expressed in blood ,Reference number: I39383; MUID:95262124; PMID:7743515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T21192 R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASCNG-----VCSPFEMP-----PCGTSAC----RCIPVGLVIGYCRNPSG 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lypothetical protein F21C3.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.3%; Score 55; DB 2; ilarity 44.4%; Pred. No. 12; Conservative 1; Mismatches 12
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A;Molecule type: mRNA
A;Residues: 1-61 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 NGDCKTFQGPNCPATCGRVLPDGKRAVVGY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 42;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NGVCSPFEMPPCGTSACRCIPVG--LVIGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, April 1996
A;Reference number: Z19388
A;Accession: T21192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 14q32.1-14q32.1
C,Superfamily: WD repeat homology
F;148-181/Domain: WD repeat homology <WDl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metallothionein II - golden hamster
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                                                                                                                                                                                                                                                                                             A;Gene: GDB:AAMP
A;Cross-references: GDB:4573993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.09
Matches 12, Conservative
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Matches 12; Conserv
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A;Molecule type: DNA
A;Mosidues: 1-375 < LEI: A;Mosidues: 1-375 < LEI: A;Mosidues: 1-375 < LEI: A;Mosidues: NIPROT: Q20002; EMBL: U46675; NID: 91166613; PID: 91166616; PIDN: AAB526
A;Experimental source: strain Bristol N2; clone F35A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9ZDB7; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1487
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angio-associated migratory cell protein - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004
C;Accession: 139383
R;Beckner, M.E.; Krutzsch, H.C.; Stracke, M.L.; Williams, S.T.; Gallardo, J.A.; Liotta,
Cancer Res. 55, 2140-2149, 1995
                                                                                                                                                                                                         diaminopimelate epimerase (dapF) RP415 - Rickettsia prowazekii
Cispeciaes: Rickettsia prowazekii
Cispeciaes: Rickettsia prowazekii
Cispeciaes: Rickettsia prowazekii
Cispeciaes: Allov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
Cispeciaesion: F71699
Rishurer 36, 133-140, 1998
Rishurer 36, 1989
Rishurer 371639
Rish
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16248
R;Leimbach, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, January 1996
A;Description: The sequence of C. elegans cosmid F35A5.
A;Reference number: Z18485
A;Accession: T16248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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C;Superfamily: gliadin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACN--CAPVQQDPCACQPQQQQPACNCAPV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.8%; Score 56; DB Best Local Similarity 40.9%; Pred. No. 28; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SCNGVCSPFEMPPCGTS-----ACRCIPV 25
       56
                                                                        18 śck--ckacrcpsckksccsccpyg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Genetics:
A,Gene: dapF; RP415
C;Superfamily: diaminopimelate epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 CGSGACASFAAGLKLGFVHSPS 234
       SCNGVCSPFEMPPCGTSACRCIPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTSACRCIPVGLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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A;Gene: CESP:F35A5.3
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Best Local S
Matches 11
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F;1982-2014/Domain: ankyrin repeat homology <AN3>F;2015-2047/Domain: ankyrin repeat homology <AN4>F;2048-2080/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                           25.3%;
                                                                                                                                                                                                           Query Match 25.3
Best Local Similarity 37.5
Matches 12; Conservative
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S42612
transmembrane protein precursor - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: $42612
R;Bierkamp, C: Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern C
A;Reference number: $42612; MUID:94128602; PMID:8297791
A;Accession: $42612
A;Accession: $42612
A;Reference number: $42612; MUID:94128602; PMID:8297791
A;Reference number: $42612
A;R
                                                                                                                                                                                                                                                                                                                                                                       S33869
Iaminin beta-2 chain precursor (version 2) - human
Nyllernate names: s-laminin
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Oct-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Date: 27-Oct-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
R;Iivanainen, A.; Vuolteenaho, R.; Sainio, K.; Eddy, R.; Shows, T.B.; Sariola, H.; Trygg
Matrix Biol. 14, 489-497, 1994
Matrix Biol. 14, 489-497, 1994
A;Title: The human laminin beta-2 chain (S-laminin): structure, expression in fetal tiss
A;Reference number: S53869
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C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Superfamily: laminin beta-2 chain #status predicted <SIG>
C;Superfamily: laminin beta-2 chain #status predicted <NAT>
F;1-32/Domain: signal sequence #status predicted <NAT>
F;33-1798/Product: laminin-type EGF-like homology <LE01>
F;347-407/Domain: laminin-type EGF-like homology <LE02>
F;410-467/Domain: laminin-type EGF-like homology <LE03>
F;410-467/Domain: laminin-type EGF-like homology <LE04>
F;522-552/Domain: laminin-type EGF-like homology <LE07>
F;733-828/Domain: laminin-type EGF-like homology <LE07>
F;837-924/Domain: laminin-type EGF-like homology <LE07>
F;877-924/Domain: laminin-type EGF-like homology <LE08>
F;927-934/Domain: laminin-type EGF-like homology <LE08>
F;927-934/Domain: laminin-type EGF-like homology <LE10>
F;027-934/Domain: laminin-type EGF-like homology <LE10>
F;027-934/Domain: laminin-type EGF-like homology <LE11>
F;1035-1140/Domain: laminin-type EGF-like homology <LE12>
F;1143-1187/Domain: laminin-type EGF-like homology <LE12>
F;1143-1187/Domain: laminin-type EGF-like homology <LE13>
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32.4%; Pred. No. 1.5e+02;
iive 5; Mismatches 16;
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                                                                                                                                                                                 14 SCSGSCKCKECKCTTCKKSCCSCCPVG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: GDB:LAMB2
A;Cross-references: GDB:132363; OMIM:150325
                                                                              SCNGVCSPFE--MPPCGTSACRCIPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-1798 <1IV>
A,Cross-references: UNIPROT:P55268
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Matches 11; Conserva
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laminin alpha-1 chain precursor - human
C;Specias: Homo sapiens (man)
C;Specias: Homo sapiens (man)
C;Specias: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; Ā34561
R;Haaparanta, T; Uitco, J; Ruoslahti, E; Engvall, E.
Matrix 11, 151-160, 1991
A;Title: Molecular cloning of the cDNA encoding human laminin A chain.
A;Reference number: S14458
A;Accession: S14458
A;Accession: S14458
A;Accession: S14458
A;Accession: S14458
A;Residues: 1-3075 < HAA>
A;Residues: 1-3075 < HAA>
A;Residues: 1-3075 < HAA>
A;Cross-references: UNIPROT:P25391
B;Cross-references: UNIPROT:P25391
A;Cross-references: UNIPROT:P25391
B;Cross-references: UNIPROT:P25391
A;Cross-references: UNIPROT:P25391

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Ajmolecule type: mRNA
Ajresidues: 1-227, FFE, 230-251, MLP, 255-418, E, 420-518, LL, 520-1022, VV, 1024-1074, VV, 1
Ajcross.references: EMBL:X58531; NID:934225; PIDN:CAA41418.1; PID:934226
Ajcross.references: EMBL:X58531; NID:934225; PIDN:CAA41418.1; PID:934226
Rjolsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, T.
Lab. Invest. 60, 772-782, 1989
Ajcritle: Human laminin: Cloning and sequence analysis of cDNAs encoding A, B1 and B2 chan
Ajreference number: A34961; MUID:89286632; PMID:2733383
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A;Gene: GDB:LAMA1; LAMA
A;Gross references: GDB:120135; OMIM:150320
A;Gross references: GDB:120135; OMIM:150320
A;Map position: 18p11.32-18p11.32
A;Map position: 18p11.32
A;Map positio
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                                                                                                                                                                                                                         4
          Length 2437;
Score 55, DB 2, Length 243
Pred. No. 1.9e+02;
5; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GVCSPFEMPPCGTSACRCIPVGLVIGYCRNPS 36
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Gaps

1;

Indels

DB 2;

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small cysteine-rich envelope protein envA precursor - Chlamydophila psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: A39499
R;Everett, K.D.E.; Hatch, T.P.
J. Bacteriol. 173, 3821-3830, 1991
A;Title: Sequence analysis and lipid modification of the cysteine-rich envelope proteins
A;Reference number: A39439
A;Accession: A39439
A;Accession: A39439
A;Statuse: preliminary
A;Molecule type: DNA
A;Residuse: 1-87 cEVE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P27606; GB:M61116; NID:g144489; PIDN:AAB61618.1; PID:g14490
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                                                                                                     Score 53.5; DE Fred. No. 23; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
24.7%; Score 53.5; DE
Best Local Similarity 34.4%; Pred. No. 23;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                 3 CNGVCSPFEMPPCGTSACRCIPVGLVIG 30
                                                                                                                                                                                                                                                                                            16 CDNKCG-CTVPCTGGSTCRCTSVGMTTG 42
                                                                                                     Query Match 24.7%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.7%;
llarity 30.2%;
Conservative
         A;Gene: PGMPM19
C;Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 SPFEMPPC-----
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Best Local Similarity
Matches 16; Conserv
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: F88369
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 24
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F;1160-1361/Domain: IVa <D00AA>
F;1162-1551/Domain: IIIa <D03A>
F;1362-1400/Domain: IIIa <D03A>
F;1362-1400/Domain: laminin-type EGF-like homology #status atypical <LEI7>
F;1403-1449/Domain: laminin-type EGF-like homology <LEI8>
F;1452-1566/Domain: laminin-type EGF-like homology <LEI9>
F;1554-2125/Domain: laminin-type EGF-like homology <LE20>
F;1554-2125/Domain: I/II, heptad repeats <D0N2>
F;1554-2125/Domain: G=1 adhesion #status predicted
F;2142-2300/Domain: g= xD0N6>
F;2142-2300/Domain: laminin G repeat homology <LG2>
F;2142-230/Momain: laminin G repeat homology <LG3>
F;239-2808/Domain: laminin G repeat homology <LG3>
F;239-2808/Domain: laminin G repeat homology <LG3>
F;239-2808/Domain: laminin G repeat homology <LG5>
F;214-2530/Momain: laminin G repeat homology <LG5>
F;214-2530/Momain: laminin G repeat homology <LG5>
F;214-2530/Momain: laminin G repeat homology <LG5>
F;38-164-555,665,763,901,803-956,952-1045,1407,1579,1596,1678,1609,1717,1804,1894,1
F;38-164-555,665,763,954-952-1045,1407,1579,1596,1678,1609,1717,1804,1894,1
Fig. (Covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:022378; EMBL:AF010186; NID:g2306978; PIDN:AAB65792.1; PID:g2
A;Experimental source: strain Shi-Shi; cotyledon
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:99360089; PMID:9693030
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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 09-ppr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05119
R;Hsu, T.F.; Tsai, F.Y.; Hsing, Y.I.; Chow, T.Y.
Submitted to the EMBL Data Library, June 1997
A;Description: Glycine max metallothionein-II protein mRNA.
A;Reference number: Z15431
A;Accession: T05719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.6e+02;
2; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.3%; Score 55; DB 2; Length 3075; Best Local Similarity 44.0%; Pred. No. 2.3e+02; Matches 11; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555 CNETCPPDTFGKNCSSPCTCONGCTCDPVLGACRCPPG 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: T13954
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1574 «NAK»
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A,Molecule type: mRNA
A,Residues: 1-85 <HSU>
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36.8%;
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T13954
MEGF6 protein - rat
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Matches 14
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A,Gene: MEGF6
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Gaps

Indels

Length 87;

DB 2; 17;

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Rjanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematods PMID:9965613; PMID:9951916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C_ele-A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n.
protein unc-52 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: Chr_II; PIDN: CAB07704.1; PID: 93881355; GSPDB: GN00020
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Pred. No. 1.6e+02;
4; Mismatches 10;
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Sequence 421, App Sequence 411, App Sequence 517, App Sequence 518322, Sequence 21, App Se
4 US-10-184-634-301

4 US-10-184-634-301

4 US-10-155-91

4 US-10-155-91

4 US-10-146-731-421

4 US-10-146-731-421

4 US-10-146-731-421

4 US-10-142-885-421

4 US-10-142-885-421

5 US-10-140-865-421

6 US-10-140-865-421

10S-09-845-534

10S-09-845-534

10S-09-845-531-6

10S-09-845-70-70-10

10S-09-845-70-70-10

10S-09-845-70-70-10

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        Sequence 167170,
Sequence 210838,
Sequence 12, Appl
Sequence 269230,
Sequence 117, Appl
Sequence 113, App
Sequence 313, App
Sequence 313, App
Sequence 213, App
Sequence 225, Appl
Sequence 225, App
Sequence 225, App
                                                                                                                                                                          March 28, 2005, 09:00:16; Search time 68.5 Seconds (without alignments) 178.843 Million cell updates/sec
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Published Applications Asia.

1. (cgn2_6/ptodata/2/pubpaa/USOT PUBCOMB.ppp:*

1. (cgn2_6/ptodata/2/pubpaa/USOT NEW PUB.ppp:*

1. (cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.ppp:*

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1. (cgn2_6/ptodata/2/pubpaa/USOB_NEW PUB.ppp:*

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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-424-599-210838
US-09-782-130-12
US-09-782-130-12
US-09-782-130-17
US-10-184-644-313
US-10-184-644-313
US-10-164-634-313
US-10-065-685-101
US-10-065-685-101
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US-10-184-644-301
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Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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Score

Result No.

Post-processing: Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Sequence:

protein -

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Run ĕ

Scoring table:

Total number

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APPLICANT: KNAUF, VIC C.
APPLICANT: KNAUF, VIC C.
APPLICANT: KRIDL, JEAN C.
1TILE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION
1TILE OF INVENTION: METHODS AND EXPRESSION OF HETEROLOGOUS GENES
FILE REFERENCE: 16518.052
CURRENT APPLICATION NUMBER: US 09/232,861
PRIOR APPLICATION NUMBER: US 09/232,861
PRIOR APPLICATION NUMBER: US 09/232,861
PRIOR APPLICATION NUMBER: US 08/484,941
PRIOR APPLICATION NUMBER: US 08/484,941
PRIOR APPLICATION NUMBER: US 08/484,941
PRIOR PLILNG DATE: 1995-06-07
PRIOR PLILNG DATE: 1995-06-07
PRIOR PLILNG DATE: 1995-06-10
PRIOR PPLICATION NUMBER: US 07/526,123
PRIOR PLILNG DATE: 1990-06-22
PRIOR PLILNG DATE: 1990-06-10
PRIOR PLILNG DATE: 1990-06-14
PRIOR PLILNG DATE: 1980-11-02
PRIOR PLILNG DATE: 1980-11-07
PRIOR PLILNG DATE: 1980-01-17
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US-09-782-130-12
                                                                                                                                                             46.5%; Score 101; DB 15; Length 80;
43.2%; Pred. No. 0.0013;
tive 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.6%; Score 88; DB 11; Length 18; Best Local Similarity 72.2%; Pred. No. 0.0092; Matches 13; Conservative 3; Mismatches 2; Indels
                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32413C.l.pep
US-10-424-599-210838
                                                                                                                                                                                                                                                                                      1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                                                                                                                                                                                                                                                                                                                              28 ADCIGSCTSFYIPPCLSRDCRSVSIXLITGFCHPSG 64
      OTHER INFORMATION: unsure at all Xaa locations
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; BENEAL INFORMATION:
; APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09782130 Publication No. US20040055038A1 GENERAL INFORMATION:
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                                                                                                                                                             Query Match
Best Local Similarity 43.23
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-269230
                                    FEATURE:
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Publication No. US20040031072A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: APPLICANT: Are avid K

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION PUMBER: US/10/424,599

CURRENT APPLICANTON NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

INRGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-167170, Application US/10424599

Sequence 167170, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICANTION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ENGINE 
                                                              Sequence 4, Appli
Sequence 271846,
Sequence 77, Appl
Sequence 283, Appl
Sequence 29453, Appl
Sequence 161876,
Sequence 161876,
Sequence 160854,
Sequence 269, Appl
Sequence 269, Appl
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                                       Sequence 191209,
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                          5 US-10-424-599-191209
6 US-10-611-527-4
5 US-10-424-599-271846
0 US-09-825-751A-77
0 US-09-989-920-283
1 US-09-864-408A-3966
4 US-10-029-386-29453
6 US-10-108-260A-4652
6 US-10-437-963-161876
6 US-10-437-963-161876
6 US-10-437-963-160854
6 US-10-437-963-160854
6 US-10-625-586-269
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                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-174-590-269
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ORGANISM: Glycine max
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LOCATION: (1)..(80)
   RESULT 2
US-10-424-599-210838
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   TYPE: PRT
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16 GTSACRCIPVGLVIGYCR 33
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Best Local Similarity 72.2%;
Matches 13; Conservative
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ilarity 34.1%;
Conservative
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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us-09-674-

"FLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 269230

LENGTH: 101

TYPE: ...
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WS-09-782-130-17

WS-09-782-130-17

Sequence 17, Application US/09782130

PUBLIcation No. US20040055038A1

GENERAL INFORMATION:

APPLICANT: KNAIDL, JEAN C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION

TITLE OF INVENTION: METHOD SATE: 2001-02-12

CURRENT APPLICATION NUMBER: US/09/782,130

CURRENT APPLICATION NUMBER: US 08/232,861

PRIOR PILING DATE: 1990-01-15

PRIOR PILING DATE: 1990-01-15

PRIOR PLING DATE: 1990-06-10

PRIOR PLING DATE: 1990-06-10

PRIOR APPLICATION NUMBER: US 08/105,852

PRIOR APPLICATION NUMBER: US 07/256,123

PRIOR APPLICATION NUMBER: US 07/256,123

PRIOR PLING DATE: 1990-05-21

PRIOR PLING DATE: 1990-05-21

PRIOR PLING DATE: 1990-05-21

PRIOR PLING DATE: 1990-05-21

PRIOR PLING DATE: 1990-05-14

PRIOR PLING DATE: 1990-05-14

PRIOR PLING DATE: 1990-09-14

PRIOR PLING DATE: 1990-03-15

PRIOR PLING DATE: 1990-03-15
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US-09-782-130-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_85135C.1.pep
US-10-424-599-269230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(101)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 13; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430ALC227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Tahy, Edin D.
APPLICANT: Tahy, Edin D.
APPLICANT: Tahy, Edin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Harnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088.465
CURRENT APPLICATION NUMBER: US.03-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1481
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Pred. No. 80;
4; Mismatches 15; Indels 10
DB 11; Length 18;
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NUMBER OF SEQ ID NOS: 612
Score 75; DB 11
Pred. No. 0.22;
                                                    1; Mismatches
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LENGTH: 1798
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P943-0917-217 CURRENT APPLICATION NUMBER: 105/10/184,634 CURRENT FILING DATE: 2002-06-28
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ch 30.0%; Score 65; DB 14; Length 1728; Similarity 34.4%; Pred. No. 1.2e+02; 11; Conservative 2; Mismatches 19; Indels
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LENGHH: 1728
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Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                    ; Sequence 313, Application US/10184634; Publication No. US20030068684A1; GENERAL INFORMATION:
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Publication No. US20030180909A1;
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvareff, Ellen
APPLICANT: Gerritsen Mary E.
APPLICANT: Gerritsen Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe, Colin K. Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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; ORGANISM: Homo Sapien
; US-10-063-685-101
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; ORGANISM: Homo Sapien
US-10-184-634-313
                          Local Similarity
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       Query Match
                              Best Loca
Matches
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CURRENT APPLICATION NUMBER: US/10/184,644

CURRENT FILING DATE: 2002-06-28
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    Length 1728;
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                                                                                                                                                                                                                                                                              GENERAL INC. USZCUZZIĄ SPĄAI

GENERAL INFORMATION:

APPLICANT: Burgeson, Robert

APPLICANT: Burgeson, Robert

APPLICANT: Champliand, Marie-France

APPLICANT: Hunter, Dale

TITLE OF INVENTION: LAMININ 15 AND USES THEREOF

FILE REFERENCE: 10287-056001

CURRENT APPLICATION NUMBER: US/09/845,583

CURRENT PILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: US 60/200,863

PRIOR APPLICATION NUMBER: US 60/200,863

PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 18

SOFTWARE: FastSEQ for Windows Version 4.0
Score 65; DB 14;
Pred. No. 1.2e+02;
2; Mismatches 19
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Pred. No. 2.7e+02
4; Mismatches 1
                                                                                           1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYC 32
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Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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Patent No. US20020142954A1
  Query Match
Best Local Similarity 34.4%;
Matches 11; Conservative ;
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Best Local Similarity 36.4%;
Matches 12; Conservative
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Godowski, Paul J.
Gurney, Austin L.
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ORGANISM: Homo sapiens
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US-10-184-644-225
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REPERBNCE: P343031C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zelliam I.
APPLICANT: Zhang, Zelliam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184, 644
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  Indels
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  15;
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Best Local Similarity 37.5%; Pred. No. 5.5e+02;
Matches 12; Conservative 2; Mismatches 15
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                                           1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYC 32
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  2; Mismatches
                                                                                        350 Arceccereccrecirrereare
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Watanabe, Colin K.
Wood, William I.
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Gurney, Austin L.
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Godowski, Paul J.
Gurney, Austin L.
12; Conservative
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ORGANISM: Homo Sapien
US-10-184-634-225
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; ORGANISM: Homo Sapien
US-10-184-644-301
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APPLICANT: Grandldi, Christopher J.
APPLICANT: Grandldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 170
SEQ ID NO 91
LENGTH: 1871
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 1943.0811.0217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                             Gaps
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Score 60; DB 14; Length 1871;
Pred. No. 4.6e+02;
3; Mismatches 16; Indels 6
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Pred. No. 4.6e+02;
3; Mismatches 16; Indels 6
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 301
                                                                                                                                                           490 ATCAGCCT-----CGTGCCCCCCAGTAAAGCTGTAG 520
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     Query Match 27.6%;
Best Local Similarity 32.4%;
Matches 12; Conservative
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Goddard, Audrey
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Best Local Similarity 32.44
Matches 12, Conservative
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Smith, Victoria
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ORGANISM: Homo Sapien
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ORGANISM: Homo Sapien
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Gaps

Matches

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT PILING DATE: 2020-05-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 1355
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333001C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
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Pred. No. 3.9e+02;
2; Mismatches 20; Indels 1;
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 421
LENGTH: 1355
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Publication No. US20030138888A1
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US-10-141-761-421
; Sequence 421, Application US/10141761
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Best Local Similarity 37.8%;
Matches 14; Conservative
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                                 Watanabe, Colin K
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Gerritsen, Mary E.
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Watanabe, Colin K
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Sherwood, Steven
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; ORGANISM: Homo Sapien
US-10-140-472-421
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; ORGANISM: Homo Sapien
US-10-146-731-421
                            APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.C30
CURRENT PAPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 421
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                                                  Length 1871;
                                          27.6%; Score 60; DB 14; Length 18
32.4%; Pred. No. 4.6e+02;
tive 3; Mismatches 16; Indels
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Publication No. US20030068794A1
GENERAL INFORMATION:
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Publication No. US20030129692A1
GENERAL INFORMATION:
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Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Filvaroff, Ellen
                                                                                        12, Conservative
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ORGANISM: Homo Sapien
                                          Query Match
Best Local Similarity
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US-10-063-685-91
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APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.C448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
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                                                             Score 59.5; DB 14; Length 1355;
Pred. No. 3.9e+02;
2; Mismatches 20; Indels 1;
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Pred. No. 3.9e+02;
2; Mismatches 20; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550 SEQ ID NO 421
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                                                               Query Match 27.4%;
Best Local Similarity 37.8%;
Matches 14; Conservative
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Matches 14; Conservative
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Filvaroff, Ellen
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Gurney, Austin L
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       ; ORGANISM: Homo Sapien
US-10-142-885-421
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; ORGANISM: Homo Sapien
US-10-158-790-421
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FOLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C198
CURRENT APPLICATION NUMBER: US/10/141, 761
CURRENT FILING DATE: 2002-05-08
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Publication No. US20030157604A1
GENERAL INFORMATION:
tion No. US20030148432A1
INFORMATION:
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Gurney, Austin L.
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Filvaroff, Ellen
Gao, Wei-Qiang
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Filvaroff, Ellen
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                                                                                 DeForge, Laura
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                                             APPLICANT: Baker, Kevin P.
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ORGANISM: Homo Sapien
US-10-141-761-421
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.1210/140,923
CURRENT APPLICATION NUMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1G1S
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT PILING DATE: 2002-05-03
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27.4%; Score 59.5; DB 15; Length 1355;
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1;
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Stewart, Timothy A.
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Wood, William
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DeForge, Laura
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                       Tumas, Daniel
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CRGANISM: Homo Sapien
US-10-140-923-421
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ORGANISM: Homo Sapien
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US-10-140-923-421
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APPLICANT:
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RESULT 24 , US-10-141-756-421

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C197
CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 421
LENGTH: 1355
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SCIENCE ENCODING THE SAME
FILE REFERENCE: P3330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 1355
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Pred. No. 3.98+02;
2; Mismatches 20; Indels 1;
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Publication No. US20030207361A1
GENERAL INFORMATION:
Sequence 421, Application US/10141756
Publication No. US20030207359A1
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Best Local Similarity 37.8%;
Matches 14; Conservative
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Watanabe, Colin K
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Wood, William
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Gerritsen, Mary E.
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Gurney, Austin L.
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Desnoyers, Luc
Filvaroff, Ellen
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; ORGANISM: Homo Sapien
US-10-141-756-421
                              Publication No. US20
GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-759-421
Query Match
Best Local Similarity 37.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 2; Mismatches 20; Indels 1; Gaps
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Search completed: March 28, 2005, 09:15:18 Job time : 69.5 secs

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US-09-125-091A-20055
US-09-252-991A-20055
US-09-252-991A-22898
US-09-252-991A-22898
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US-09-252-991A-22898
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US-09-627-650B-3
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US-09-627-650B-9
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US-09-252-991A-23483
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-08-327-925-5
US-08-828-584-8
US-09-845-583A-8
US-09-917-254-87
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US-08-460-309-5
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                              GenCore version
Copyright (c) 1993 - 2005
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Listing first 100 summaries
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| Bedent No. 6812339 |
| GENERAL INFORMATION |
| FAPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| WUMBER OF SEQ ID NOS: 207012 |
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Pred. No. 18;
4; Mismatches 15; Indels ::
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
FILING DATE:
ALIGNMENTS
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NAWE: POSCISSE, Laurence H.
RECISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEPHAX: 202 508-9299
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Best Local Similarity 34.1
Matches 15; Conservative
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ORGANISM: Human
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Sequence 5, Application US/08828584
Patent No. 5908762
GENERAL INFORMATION:
GENERAL SECONDER ON, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Retroviral Expression Contructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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Pred. No. 19;
4; Mismatches 15; Indels
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Pred. No. 19;
4; Mismatches 15; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Banner, Birch, McKie & Beckett STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia COUNTRY: U.S.A.
ZIP: 2000 TER: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWAKE: FALCHLIH KATGAGE TOO, CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,584
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: POSOTSK, LAURENCE H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.46362
TELEPHONE: 20-2 508-9153
TELEPHONE: 20-2 508-9153
TELEPHONE: 20-2 508-9153
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                                                                                                                                                                                                                                                                                                                                30.0%;
34.1%;
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Best Local Similarity 34.1%;
Matches 15; Conservative
                                                                                   1104 amino acids
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.14
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                      TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: protein

US-08-327-832-5
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-845-583A-8
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US-08-828-584-5
                                                                                       LENGTH:
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Gape

7

Indels

15;

DB 4; Length 1798;

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Score 62; DB 4
Pred. No. 65;
4; Mismatches
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFFMARE: PatentIn version 3.0
SEQ ID NO 87
LENGTH: 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                               Query Match 28.6%;
Best Local Similarity 36.4%;
Matches 12; Conservative 4
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US-09-902-540-15052
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Best Local Similarity 32.33
Matches 10; Conservative
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US-09-917-254-87
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US-09-252-991A-20537
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                                                                                                                               TYPE: PRT
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APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (GRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 4; Length 1798;
Pred. No. 65;
4; Mismatches 15; Indels
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             APPLICANT: Bruyesu, ADDEL
APPLICANT: Bruyesu, ADJES
APPLICANT: Champliaud, Marie-France
APPLICANT: Champliaud, Marie-France
APPLICANT: Champliaud, Marie-France
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
FILE REFERENCE: 10287-056001
CURRENT APPLICATION NUMBER: US/09/845,583A
CURRENT FILING DATE: 2001-04-30
PRIOR PLING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burgeson, Robert
APPLICANT: Champliaud, Marie-France
APPLICANT: Champliaud, Marie-France
APPLICANT: Olson, Pamela
APPLICANT: Koch, Manuel
APPLICANT: Roch, Malliam
ITILE OF INVENTION: LAMININS AND USES THEREOF
FILE RFERENCE: 10287-060001
CURRENT FILING DATE: 2000-05-01,
PRIOR APPLICATION NUMBER: US 09/168,949
PRIOR APPLICATION NUMBER: US 09/168,949
PRIOR PILING DATE: 1998-10-09
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1:
LENGTH: 1798
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; Pred. No. 65;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09561709B; Patent No. 6682911; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 87, Application US/09917254; Patent No. 6703204; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.6%;
Best Local Similarity 36.4%;
Matches 12; Conservative
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Best Local Similarity 36.4%;
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-561-709B-11
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-561-709B-11
                                                                                                                                                                                                                                                                              LENGTH: 1798
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Sequence 20537, Application US/09252991A

Sequence 20537, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

JERUS OF INVENTION: MUCLEIC ACID ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 210
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                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 06/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PLILING DATE: 2001-07-10
PRIOR PLILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15052
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                                                      816 CAPGYYGFGPTGCQACQCSPRGALSSLCERTSG 848
7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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                                                                                                                                                                                             Sequence 15052, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
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Best Local Similarity

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Query Match 27.0%; Score 58.5; DB 4; Length 1761; Best Local Similarity 41.9%; Pred. No. 1.6e+02; Matches 18; Conservative 2; Mismatches 10; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SC--NGVCSPFEMPPCG-----TSACRCIP--VGLVIGYC 32
                                                                                                                              GENERAL INFORMATION:
APPLICANT: Burgeson, Robert
APPLICANT: Champliaud, Marie-France
APPLICANT: Champliaud, Marie-France
APPLICANT: Colon, Pamela
APPLICANT: Koch, Manuel
APPLICANT: Brunken, William
TITLE OF INVENTION: LAMININS AND USES THEREOF
FILE REFERENCE: 10287-060001
CURRENT APPLICATION NUMBER: US/09/561,709B
CURRENT APPLICATION NUMBER: US 09/168,949
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 60/061,609
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                      Sequence 1, Application US/09561709B
Patent No. 6682911
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Best Local Similarity 41.74
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: LASSALLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-706-722A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 1761
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                              Gaps
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41.9%; Pred. No. 1e+02;
iive 2; Mismatches 10; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.2%; Score 59; DB 4; Length 1799; 35.3%; Pred. No. 1.46+02; ive 4; Mismatches 16; Indels
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                                                                                                                                                                                                                                                               GENERAL INTORNATION:
APPLICANT: Burgeson, Robert
APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
APPLICANT: Champliaud, Marie-France
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
FILE REFERENCE: 10287-056001
CURRENT APPLICATION NUMBER: US 60/200,863
CURRENT FILING DATE: 2001-04-30
PRIOR PILICATION NUMBER: US 60/200,863
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Burgeson, Robert
APPLICANT: Champliand, Marie-France
APPLICANT: Champliand, Marie-France
APPLICANT: Olson, Pamela
APPLICANT: Olson, Pamela
APPLICANT: Roch, Manuel
APPLICANT: Brunken, William
TITLE OF INVENTION: LAMININS AND USES THEREOF
FILE REFRENCE: 10287-060001
CURRENT APPLICATION NUMBER: US/09/561,709B
CURRENT APPLICATION NUMBER: US 09/168,949
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VCSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
57.7%; Pred. No. 13;
tive 1; Mismatches
                                                                                                              106 ASCSTTCS--TPPPCG-SACRDWPSG 128
                                                                    1 ASCNGVCSPFEMPPCGTSACRCIPVG 26
                                                                                                                                                                                                                          Sequence 6, Application US/09845583A Patent No. 6635616
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Best Local Similarity 41.9%;
Matches 18; Conservative
                     15; Conservative
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Matches 12; Conservative
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, ORGANISM: Mus musculus
US-09-845-583A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                  RESULT 9
US-09-845-583A-6
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LENGTH: 17
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                     Matches
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Gaps

13;

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APPLICANT: MARCHANDISE, GENEVIEVE
APPLICANT: MARCHANDISE, GENEVIEVE
APPLICANT: MARCHANDISE, GENEVIEVE
APPLICANT: KERVOAZE, GWENOLA
APPLICANT: TONNEL, ANDRE BERNARD
APPLICANT: MOLLET, SOPHIE
TITLE OF INVENTION: THEIR USES IN THE TREATMENT AND DIAGNOSIS OF DISEASES
TITLE OF INVENTION: LINKED TO LEUKOCYTE MIGRATION
FILE REFERENCE: 8425/P-61263US2
CURRENT APPLICATION WUMBER: US/09/706,722A
FRIDE REPLIANG DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALCHING US: 10
SOFTWARE: PALCHING US: 10
SEQ ID NO 10
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 165;
19;
12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.7%; Score 58; 41.7%; Pred. No.
                                                                                                          sequence 10, Application US/09706722A
Patent No. 6670328
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ښ</u>
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                                                                                                        ### Sequence 9, Application US/08836686B
### Patent No. 6239106
### Sequence 9, Application US/08836686B
### Sequence 9, Application US/08836686B
### Sequence 9, Application US/08836686B
### TITLE OF INVENTION: A novel family of protease inhibitors, and other
### TITLE OF INVENTION: Biologic active substances
### TITLE OF INVENTION: Biologic active substances
### CURRENT APPLICATION NUMBER: US/08/836,686B
### CURRENT FILING DATE: 1994-03-27
### PRIOR FILING DATE: 1994-10-28
### PRIOR PILING DATE: 1995-03-14
### PRIOR FILING DATE: 1995-03-14
### PRIOR PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(41)
; OTHER INFORMATION: sequence of another isoform, which was found to be
; OTHER INFORMATION: a mixture of two molecules, in peak 9 (figure 7)
US-08-836-686B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NCGGQVCSKGQL--CVDGQCKCTPIRCLI-YCPN 33
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Best Local Similarity 36.7%; Pred. No. 23;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CSPFEMPPCGTSACRCIPVGLVIGYCRNPS 36
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; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Limnatis nilotica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
US-09-252-991A-17204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 41
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Sequence 24124, Application US/09252991A

Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ACCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PRING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28424

LENGTH: 998
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Worley, Paul F.
APPLICANT: Lanahan, Anthony
APPLICANT: Lanahan, Anthony
APPLICANT: George, Bernard
APPLICANT: George, Bernard
APPLICANT: George, Bernard
APPLICANT: George, Bernard
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Thikoloh, Karoly
APPLICANT: THEREOR
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE 1999-02-05
FILE REFERENCE: 10496/004001
CURRENT FILING DATE: 1999-02-05
FRIOR APPLICATION NUMBER: 60/074,518
FRIOR APPLICATION NUMBER: 60/074,518
FRIOR PRILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PASHESEQ FOR Windows Version 4.0
SEQ ID NO 27
LENGTH: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.5%; Score 57.5; DB 4; Length 581; 34.1%; Pred. No. 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 71;
3; Mismatches 17; Indels
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54 PAGCQACQCSPDGALSALCEGTSG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PFEMPPCGTSACRCIPVGLVIGY 31
                                                                                                                                                                                                                           Sequence 27, Application US/09244805
Patent No. 6699660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Eukaryote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-252-991A-28424
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US-09-244-805-27
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Gaps 5

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Query Match 25.8%; Score 56; DB 5; Length 415; Best Local Similarity 40.0%; Pred. No. 77; Matches 12; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                           205 NGDCKTFQGPNCPATCGRVLPDGKRAVVGY 234
                                                                                                                                                                                                                                                                                                                                      4 NGVCSPFEMPPCGTSACRCIPVG--LVIGY 31
REFERENCE/DOCKET NUMBER: 15280-156-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application PC/TUS9407107A GENERAL INFORMATION:
    INFORMATION:

TELEFAX: (415) 326-2402

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                 MOLECULE TYPE: protein
PCT-US94-07107A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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Pred. No. 77;
4; Mismatches 12; Indels
                                                                                                                                                                                                                  COMPURY: D.C.

COMPURY: USA

ZIP: 2005-3918

COMPUTER READABLE FORM:
MEDITUR TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin PCT/US93/00601
PILING DATE: 19930129
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (202) 862-0944
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENTY #15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9407107A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of
APPLICANT: America, as represented by the Secretary,
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07107A
FILING DATE: 25-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 NGDCKTFQGPNCPATCGRVLPDGKRAVVGY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 NGVCSPFEMPPCGTSACRCIPVG--LVIGY 31
                        APPLICANT: Beckner, Marie E.
APPLICANT: Liotta, Lance A.
TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEB: CUSHMAN, DARBY & CUSHMAN STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-JUN-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  ; Sequence 2, Application PC/TUS9300601
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 415 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 40.0%
....hes 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94301
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PCT-US94-07107A-2
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APPLICANT: The Government of the United States of APPLICANT: America, as represented by the Secretary, APPLICANT: Department of Health and Human Services TITLE OF INVENTION: AAMP-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                          COMPUTER KELMABLE FURDEY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/07107A
FILING DATE: 25-UM-1993
CLASSIFICATION NUMBER: US 07/827,043
FILING DATE: 29-JAN-1992
ATPOINTEY/AGENT INFORMATION:
NAME: DOW, KAREN B.
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 236-2400
TELEPHONE: (415) 236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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Gaps
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,945C
FILING DATE: 25-JUN-1993
CLASSIFICATION NUMBER: US/08/083,945C
FILING DATE: 25-JUN-1993
CLASSIFICATION NUMBER: US/08/083,945C
FILING DATE: 25-JAN-1993
CLASSIFICATION NUMBER: US/08/043
FILING DATE: 29-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELEPHONE: (415) 326-2420
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
T-DNGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08785530

Fatent No. 5814480

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304

COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESE for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,530
FILING DATE: Herewith
CLASSIFICATION: 514
PRICR APPLICATION 514
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 NGDCKTFQGPNCPATCGRVLPDGKRAVVGY 245
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Pred. No. 82;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.8%;
Best Local Similarity 40.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
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CA
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08083945C
| Patent No. 6274134
| GENERAL INFORMATION:
| APPLICANT: Beckner, Marie E. APPLICANT: Liotta, Lance A. APPLICANT: Krutzsch, Henry C. 1TTLE OF INVENTION: AAMP-1. NUMBER OF SEQUENCES: 15
| CORRESPONDENCE 105
| APPLICANT: Trutz Chinaman Canada Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,945C
FILING DATE: 25-070-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,043
FILING DATE: 29-0AN-1992
ATTORNEY/AGRAT INFORMATION:
NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                              Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 NGDCKTFQGPNCPATCGRVLPDGKRAVVGY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DOW, KATER B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-156-1
TELECOMINICATION INFORMATION:
TELEPRONE: (415) 326-2400
TELEPRONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 NGVCSPFEMPPCGTSACRCIPVG--LVIGY 31
                                                                                                                                                                                                                                                                                                                     STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTR: US
ZIP: 94301
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                            US-08-083-945C-2
; Sequence 2, Application US/08083945C
; Patent No. 6274134
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Beckner, Marie E.
APPLICANT: Liotta, Lance A.
APPLICANT: Krutzsch, Henry C.
TITLE OF INVENTION: AAMP-1
CUMBER OF SEQUENCES: 15
CNESSPONDENCE ADDRESSE:
ADDRESSEE: Townsend and Towns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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STATE: California
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Sequence 15, Application US/08460309
Patent No. 5837496
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Best Local Similarity 44.0
Matches 11, Conservative
                                                                                                                                                                                                                           CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                  92122
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                                                                                                                                            DB 2; Length 61;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09123850

Sequence 6, Application US/09123850

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRSELSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/123,850
                                                                                                                                          25.3%; Score 55; DB 44.4%; Pred. No. 16; Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0194 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SCNGVCSPFE--MPPCGTSACRCIPVG 26
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
           STRANDEDNESS: Single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: GenBank
CLONR: 305363
US-08-785-530-6
                                                                                                                                                           Best Local Similarity 44.49
Matches 12, Conservative
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Best Local Similarity
Matches 12; Conserva
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amino acid
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; CLONE: 305363
US-09-123-850-6
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                                                                                                                                                                                                                                                                                                                          US-09-123-850-6
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STATE:
                                                                                                                                            Query Match
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Sequence 15, Application US/08460309

SERENT NO. 237496

CARREAL INFORMATION: Production of the process of the
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Query Match 25.3%; Score 55; DB 2; Length 243; Best Local Similarity 44.0%; Pred. No. 60; Matches 11; Conservative 2; Mismatches 10; Indels
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STRTE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATPRING MAPELICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATPRING MAPELICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATPRING MAPELICATION NUMBER: 31,815
FILING DATE: 27-JUL-1992
ATPRING MAPELICATION NUMBER: 31,815
FECINATION NUMBER: 31,815
FELECOMMUNICATION NUMBER: 31,815
FECINATION NUMBER: 31,815
FELECOMMUNICATION NUMBER: 31,815
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118 SPYEDEPC--RPCNCDPVGSLSSVC 140 8 SPFEMPPCGTSACRCIPVGLVIGYC 32 ઠે 셤

Gaps

Search completed: March 28, 2005, 09:02:15 Job time : 31 secs

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Aam50359 Mouse lam Ada17495 Amino aci Adr97664 Murine la Ade08939 Novel pro Adn04730 Antipsori	Ade28641 Human NOV Adm93386 Human NOV Aay15459 SEQ ID 5 Ade07851 Novel pro Aay15457 Human lam	Adm24888 Laminim b Abm85168 Mouse pro Aaw50895 Rat lamin Ade60383 Rat Prote	Aay42//4 kat neuro Aam51819 kat apopt Abj38280 pAMG21-RA	Aari2095 Antigenic Ab58802 Drosophil	Adp30525 Human sec Aar24045 Apolipopr Adj92151 Human hai Abo79678 Pseudomon	Abb66566 Drosophil Abo68458 Peeudomon Aaul636 Human nov Abb55605 Human nov	Abb68017 Drosophil Aar3292 AAMP-1, 1 Aar66773 N-termina Aar66776 Cell adhe Abm80393 Tumour-as Adr73434 Human ang Aau82968 Human hom Abg99510 Conus sp	Aau45020 Propionib Abm41539 Propionib Abm74267 DNA clone Aag71666 Human Olf Aag72405 Human OR-	Adp30515 Human sec Adg37736 Human nov Aau66727 Propionib Aau82806 Propionib Abm48525	Abm63246 Propionib Abm49953 Propionib Abm49953 Propionib Abm49953 Propionib Abm49953 Propiide # Abb28658 Peptide # Abb28658 Peptide # Abb28658 Peptide # Abb28669 Protein # Abm4608 Human bon Aam67014 Human bon Aam67014 Human bon Aam6259 Peptide # Abg36671 Human pep Abv70429 Human adi Abw00786 Human adi Abg09754 Novel hum Adr16784 Human Nov Adr23916 Novel hum Adr2284 Human nov Adr33168 Novel hum Adr2294 Human pro Adr31068 Human pro Adr31058 Human pro Adr639156 Human pro Adr639156 Human pro Adr639158 Human pro Adr639158 Human pro
										6 ABM63246 4 AAM13434 4 ABM49353 4 AAM14874 4 ABM28658 4 ABM28658 4 AAM7301 4 AAM74608 4 AAM74608 4 AAM74608 4 AAM700786 4 AAM700786 4 AAM700786 6 ABM700786 6 ABM70259 5 ADM16784 8 ADM72284 7 ADM72284 8 ADM72284 8 ADM72284 7 ADM72284 8 ADM72284 8 ADM72284 8 ADM72284 7 ADM72284 8 ADM72284 8 ADM72284 8 ADM72284 8 ADM72284 8 ADM72284 7 ADM60896 7 ADM60896
1799 1799 1799 885	1101 1101 1105 1670 1761	165 413 1801 1801	581 7285	1579	4360 152 271 998	56 117 141 141	9377 415 415 426 452 611 92	137 137 238 318 318	1676 1676 76 76	76 142 162 162 162 162 162 162 162 163 163 164 164 164 165 164 165 165 165 165 165 165 165 165 165 165
27.2 27.2 27.2 20.72	27.0 27.0 27.0 27.0	26.7 26.7 26.7	266.5	26.33	26.03 26.03 26.03	255.8 255.8 25.8 25.8 3	22222222 22222222 222222222 222222222 2222	25.55.6 25.6.6.6.6	22 22 23 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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5.1.6 Compugen Ltd.	Search time 92 Seconds (without alignments) 155.545 Million cell updates/sec	IGYCRNPSG 37			2105692 		·	cted by chance to have a of the result being printed,	iscribucion. Descript	O
GenCore version 5.1 Copyright (c) 1993 - 2005 Com protein search, using sw model	search, using sw model h 28, 2005, 08:39:59 ;	496D-6 :SPFEMPPCGTSACRCIPV	: 21/ 1 ASCNGVCSPFEMPPCGTSACRCIPVGLVI : BLOSUM62 Gapop 10.0 , Gapext 0.5 2105692 BedB. 386760381 residue	2105692 seqs, 386760381	oi nics satisiying chosen parameters q length: 0 q length: 200000000	ength: Minim Maxim Listi	A_Geneseq_16Dec04;* 1: geneseqp1980s;* 2: geneseqp2000s;* 4: geneseqp2001s;* 5: geneseqp2001s;* 6: geneseqp2003as;*		# Query Match Length DB	100.0 37 3 99.5 71.0 37 3 71.0 37 3 71.0 37 3 37 3 30 0 1024 5 30 0 1024 5 28 6 108 6 28 6 1798 5 28 6 1798 5 28 1 28 1 28 1 30 0 1104 2 28 8 4 9 5 28 8 28 8 1798 5 28 1 28 1 30 3 28 1 30 3 28 1 30 3 30
	OM protein - Run on:	Title: Perfect score Sequence:	Scoring table	hed:	Total number of Minimum DB seq Maximum DB seq	Post-processing:	Database :	Pred. N	2 8	

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AAY55992;
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AAY55992
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Aaw50892 Human lam
Adi34568 Human ins
                                                                                                 Consensus; plant, legume; insecticide; entomotoxic; pea; cereal; grain; pest; Sitophilus oryzae; Ephestia kuehniellea; Acyrthosiphon pisum; genetically modified organism.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                       Length 37;
                                                                                                                                                                                                      Mbailao
                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                     Ferrasson E,
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 217; DB 3;
100.0%; Pred. No. 6.1e-16;
ive 0; Mismatches 0;
                        ALIGNMENTS
                                                                                      Insecticidal peptide PT from pea plants.
AAW50892
ADI34568
                                                                                                                                                                                  (NASC-) INST NAT SCI APPLIQUES LYON. (INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                     Gueguen J,
                                                   AAY55990 standard; peptide; 37 AA.
                                                                                                                                                                                                                                            Example 2; Fig 7; 38pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAY55991 standard; peptide; 37
                                                                                                                                                            99WO-FR001085
                                                                                                                                                                        98FR-00005877
 0 P
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
3075
      63
                                                                                                                                                                                                    Delobel B, Grenier A,
                                                                                                                                                                                                                WPI; 2000-062304/05.
25.3
25.1
                                                                                                                                                                                                                                                                                                                                          Sequence 37 AA;
                                                                                                                         Pisum sativum
                                                                                                                                    WO9958695-A1
                                                                                                                                                           07-MAY-1999;
                                                                                                                                                                       11-MAY-1998;
                                                                           15-MAR-2000
                                                                                                                                                18-NOV-1999
55
54.5
                                                               AAY55990;
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                                       RESULT 1
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AAY55991
ID AAY5
XX
AC AAY5
100
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This sequence represents the Cys-rich peptide sequence of legume plant derived insecticidal peptide PAID corresponding to that of an entomotoxic pea protein. The invention relates to a novel insecticidal peptide PT (AAYS5990) isolated from pea plants which has homology to the PAID peptide and to the leginsuline from soybeans (AAYS5991). The insecticidal peptide and to the leginsuline from soybeans (AAYS5991). The insecticidal peptides preferably have the amino acid sequence:

XICysX2CysX4CysX5CysX6CysX7 where XI = 2-10 amino acids; XS = 2-4 amino acids; XS = 7-15 amino acids; XA = 3-10 amino acids; XS = 2-4 amino peptide can be used to protect cereal products or plants from attack by cereal grain pests, e.g. Sitophilus oryzae, Ephestia kuehniellea or Acyrthosiphon pisum, either directly or by genetically modifying plants (especially cereal plants) to express the peptide in their tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                 Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain; pest; Sitophilus oryzae; Ephestia kuehniellea; Acyrthosiphon pisum; genetically modified organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of polypeptide as insecticide, especially for controlling cereal grain pests.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gueguen J, Ferrasson E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 216; DB 3;
Pred. No. 7.8e-16;
1; Mismatches 0;
                                                   Insecticidal peptide PAlb from pea plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NASC-) INST NAT SCI APPLIQUEES LYON.
(INRG ) INST NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                     98FR-00005877.
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15-MAR-2000 (first entry)
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Best Local Similarity 97.33
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grenier A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-062304/05.
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                                                                                                                                                                                                             Pisum sativum.
                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1999;
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01-JUL-2004 (first entry)
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Matches 13; Conservative
                                                                                                   (CALJ ) CALGENE LLC.
                                                                                                                               Knauf VC, Kridl JC;
                                                                                                                                                            WPI; 2001-564354/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                    transcription.
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            21-MAY-1990;
09-JUL-1990;
10-AUG-1993;
07-JUN-1995;
07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-1985;
31-JUL-1986;
26-MAY-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD021580;
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                                                                                                                                                                                                                                                                                      This sequence represents the Cys-rich peptide sequence of legume plant derived insecticidal peptide leginsuline corresponding to that of an entomotoxic pea protein. The invention relates to a novel insecticidal peptide protein. The invention relates to a novel insecticidal peptide professor isolated from pea plants which has homology to the PAID peptide (AAY55991) and to the leginsuline from soybeans. The insecticidal peptides preferably have the amino acid sequence: XICysXZCySXCySXCySXCySXXCySXX, where X = 2-10 amino acids; X = 2-5 amino acids; X = 4-10 amino acids; X = 2-4 amino acids; X = 7-15 amino acids; X = 2-10 amino acids; X = 2-4 amino peptides can be used to protect cereal products or plants from attack by cereal grain peets, e.g. Sitophilus orzae, Ephestia kuehniellea or Acyrthosiphon pisum, either directly or by genetically modifying plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (especially cereal plants) to express the peptide in their tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                   Use of polypeptide as insecticide, especially for controlling cereal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11; 2A11; PA1B.
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0
                                                                                                                                                          Mbailao M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.0%; Score 154; DB 3; Length 37
59.5%; Pred. No. 2.8e-09;
ive 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYCRNPSG 37
                                                                                                                                                            Ferrasson E,
                                                                                                              (NASC-) INST NAT SCI APPLIQUEES LYON.
(INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                          Gueguen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seed storage protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB85936 standard; peptide; 18 AA
                                                                                                                                                                                                                                                            Example 2; Fig 7; 38pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86US-00891529.
87US-00054369.
87US-00078538.
88US-00147781.
88US-00168190.
                                                       99WO-FR001085
                                                                                    98FR-00005877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 59.5
22; Conservative
                                                                                                                                                         Delobel B, Grenier A,
                                                                                                                                                                                       WPI; 2000-062304/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 AA;
                                                                                    11-MAY-1998;
                                                     07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-1988;
15-MAR-1988;
29-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                          18-NOV-1999
                                                                                                                                                                                                                                    grain pests
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28-JUL-1987
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The invention provides a method for obtaining a plant which produces at least one seed having a modified phenotype. The method involves transforming a host plant cell with a DNA construct which consists of perably linked components in the direction of transcription, a promoter region from a Brassica plant gene, a DNA sequence of interest other than the native conding sequence, and a transcription termination region. The method is useful for obtaining plants having modified phenotype or for altering the phenotype of a plant seed or tissue. The DNA constructs are used in manipulating plant cells to provide for regulated transcription, cused in manipulating plant cells to provide for regulated transcription, cuch as light inducible transcription, in a plant tissue or plant part of interest at particular stages of plant growth or in response to external control. These constructs are also used for modulation of expression of endogenous products as well as production of exogenous products in the seed. Sequences AABBS936-31 septement fragments of storage proteins used in comparison studies with the storage protein 2A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obtaining a plant that produces a seed with a modified phenotype or altering a seed phenotype, comprises transforming a plant cell with a I construct consisting of operably linked components in the direction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Fig 6; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VCSPFEMPPCGTSACRCI 23
88US-00267685.
90US-00526123.
90US-00550804.
93US-00105852.
95US-00484941.
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86US-00891529.
87US-00054369.
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Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11; 2A11; PA1B.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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2XXX2X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a DNA construct comprising, as operably linked components in the direction of transcription, a promoter region obtainable from a gene, e.g. a napin gene, an EAA9 gene or an acyl carrier protein (ACP) gene, a DNA sequence of interest other than the native coding sequence of the gene and a transcription termination region, where the components are functional in a plant cell and where the DNA construct is flanked by T.DNA. Also included are a plant cell having an altered phenotype as a result of expression of a DNA construct, a plant comprising a DNA construct, a seed obtained from the comprising cells comprising a DNA construct, a seed obtained from the comprising a plant having an modified phenotype or modifying the construct of a plant to impart a desired characteristic to seed as clistuct from other plant tissue, altering the phenotype of plant seed tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue and selection of plant or regulating tissue and/or developmental specific transcription and expression in plants. The plants construct, enhanced response to light and dehydration resistance and construct, and pasts. The seed specific promoters are from the plant and pasts. The seed specific promoter as from the transcription and expression in plants are firem and the fruit specific promoter as from the transcription and expression in plants are from the plant and the fruit specific promoter as from the transcription and expression in plants of the Napin, ACP and EA9 genes and the fruit specific promoter as from the transcription and expression and setting and pasts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tomato 2A11 gene. The present sequence is a reactive site from a protein similar to the tomato 2A11 protein (thought to be a protease inhibitor).
                                                                                                                                                                                                                                                                                                    New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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Pred. No. 0.015;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAlb seed storage protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB85941 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                Example 9; Fig 6; 68pp; English.
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                           88US-00168190.
88US-00188361.
88US-00267685.
90US-00526123.
90US-00582241.
                                                                                                                             93US-00105852.
95US-00484941.
97US-00812665.
99US-00232861.
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Best Local Similarity 72.2'
                                                                                                                                                                                                                                                 Kridl JC;
                                                                                                                                                                                                                                                                              WPI; 2004-247819/23
                                                                                                                                                                                                      KRIDL J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2001
 28-JUL-1987;
25-JAN-1988;
15-MAR-1988;
29-APR-1988;
                                                        02-NOV-1988;
21-MAY-1990;
09-JUL-1990;
14-SEP-1990;
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                                                                                                                                                                                                                                                 Knauf VC,
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                                                                                                                                                                                                      (KRID/)
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AAB85941
ID AAB8
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The invention provides a method for obtaining a plant which produces at least one seed having a modified phenotype. The method involves transforming a host plant cell with a DNA construct which consists of operably linked components in the direction of transcription, a promoter region from a Brassica plant gene, a DNA sequence of interest other than the native coding sequence, and a transcription termination region. The method is useful for obtaining plants having modified phenotype or for altering the phenotype of a plant seed or tissue. The DNA constructs are such as light inducible transcription, in a plant tissue or plant part of interest at particular stages of plant growth or in response to external control. These constructs are also used for modulation of expression of endogenous products as well as production of exogenous products in the seed. Sequences ABBSS94147 represent fragments of storage proteins used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining a plant that produces a seed with a modified phenotype or altering a seed phenotype, comprises transforming a plant cell with a DNA construct consisting of operably linked components in the direction of
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Pred. No. 0.35;
1; Mismatches 4; Indels
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88US-00147781.
88US-00168190.
88US-00188361.
89US-00526123.
90US-00550804.
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95US-00484941
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87US-00054369
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knauf VC, Kridl JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CALJ ) CALGENE LLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription.
Unidentified.
                                                     US6281410-B1
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Length 18;

DB 8;

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Pea, fruit specific promoter; plant; transgenic; protein storage; improved nutrient source; enhanced response to light; dehydration resistance; herbicide resistance; pest resistance; 2All gene; protease inhibitor.
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                                                                                        85US-00692605.
86US-00891529.
87US-00054369.
87US-00078538.
                                                                                                               8805-00147781

8805-00168190

8805-00188161

9005-00526123

9005-00526123

9005-00526123

9105-00105852

9105-00105852

9505-00105852

9505-00105852
                                                                             12-FEB-2001; 2001US-00782130
Pea albumin 1b N-terminus.
                                                                                                                                                                                                                 Kridl JC;
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                                                                                                                                                                                               KRIDL J C.
                                                     US2004055038-A1.
                                                                                                                                                                       07-JUN-1995
                                                                 18-MAR-2004
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02-NOV-1988
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                                                                                                                                                            08-AUG-1991
                                                                                                                                                                                                                 Knauf VC,
                                                                                                                                                                                               (KRID/)
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New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.

The invention that the direction of transcription, a promoter region obtainable from a gene, e.g. a napin gene, an EA9 gene or an acyl carrier protein (ACP) gene, an DAA sequence of interest other than the native coding sequence of the gene and a renativity to the chain the native the components are functional in a plant cell and where the DNA construct is flanked by T.DNA. Also included are a plant cell and where the DNA construct is flanked by T.DNA. Also included are a plant cell and where the DNA construct a phenotype as a result of expression of a DNA construct, a seed obtained from the phenotype of plant, bottaining a plant having a modified phenotype or modifying the comprising a plant that plant a desired characteristic to seed as genotype of a plant to impart a desired characteristic to seed as genotype of a plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue and selectively expressing a heterologous DNA sequence of a plant to impart a desired characteristic. The construct is useful in modification of plant or regulating tissue and/or construct is useful in modification of plant or regulating tissue and/or produced have increased capability of protein storage, improved nutrient source, enhanced response to light and dehydration resistance. and the Napin, ACP and EA9 genes and the fruit specific promoters are from the Napin, ACP and EA9 genes and the fruit specific promoter is from the tomato 2A11 gene and the fund to be a protein similar to the tomato 2A11 protein (thought to be a protease inhibitor). The invention relates to a DNA construct comprising, as operably linked

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Sequence 18 AA
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                                                                                                                                                                                                                                                                           Human; nuclear transcription factor 2; NFX2; chromosome 9; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human nuclear transcription factor-2 gene encoded protein, useful for
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 SCNLLCHPGPCPPCPAFMTKTCECGRTRHTVRCGQAVSVHCSNP 499
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                            4; Indels
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                                                                                                                                                                                                                                                Human nuclear transcription factor 2 (NFX2) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 5; 1
Pred. No. 1.4e+02;
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                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1 (Claims); 7pp; Chinese.
Score 75;
Pred. No.
                                                                                                                                                          ABB05595 standard; protein; 1024 AA.
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                                                                                 GSPLCRCIPAGLVIGNCR 18
                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001; 2001CN-00113502.
                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2001; 2001CN-00113502.
34.6%;
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ilarity 34.1%;
Conservative
                                                         GTSACRCIPVGLVIGYCR
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating related disease.
                              Conservative
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N-PSDB; ABA93409.
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les 15; Conserv
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1024 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou Z,
                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 9
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Query Match
Best Local Simi
Matches 13;
                                                                                                                                                                                                                   23-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2001
                                                                                                                                                                                        ABB05595;
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                                                                                                                                RESULT 8
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Human NF-X1 (AAR94957) is a new DNA-binding protein which regulates expression of major histocompatibility complex (MHC) class II molecules. The sequence was deduced from a cDNA clone (AAT18813) isolated from Raji cells. NF-X1 is a cysteine-rich polypeptide which interacts specifically with the conserved X1 box regulatory element (AAT18812) found in the proximal promoters of class II MHC genes. It contains a cysteine-rich domain (see also AAR94955-56) required for both sequence-specific binding and effector function. Overexpression of NF-X1 specifically represses transcription of the HiA-DRA gene. NF-X1 can be obtd. by expression in transformed host cells and is useful in the treatment of allergic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription factor, NF-X1 and DNA encoding it - used in regulation of MHC class II expression and in treatment of allergic disease.
                                        NF-X1; transcription factor; major histocompatibility complex; MHC; allergy; DNA-binding protein; diagnosis.
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                473. .521
/label= Cysteine-rich_repeat
533. .583
/label= Cysteine-rich_repeat
                                                                                                                                                                                                                                                                                                                                                                                              /label= Cysteine-rich_repeat
799. .839
/label= Cysteine-rich_repeat
840. .890
                                                                                                                                                                                        Cysteine-rich repeat
                                                                                                                                                                                                                               /label= Cysteine-rich_domain
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                                                                                                                                             Location/Qualifiers
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NF-X1 DNA-binding protein.
                                                                                                                                                                       417. .468
/label= Cy
                                                                                                                                                                                                           900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ono SJ, Strominger JL;
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N-PSDB; AAT18813.
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Best Local Similarity
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                                                                                                       Homo sapiens
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                                                                                                                                                                   Region
                                                                                                                                                                                                           Domain
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ABB64668
  AX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic,
                                                                           Huntington's disease; osteoarthitis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                     Human heat mitochondrial protein as a therapeutic target SeqID1481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                            mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SCNGVCSPFEMPPCG---TSACRC----IPVGLVIG-YCRNP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1481; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2002; 2002US-0389987P.
                                                                                                                                                                                                                                                                                                                                                   04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                              .2-APR-2002; 2002US-0372843P.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1024 AA;
                                                                                                                                                                                                                                                                     4O2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                             7-JUN-2002;
                                                                                                                                                                                                                               Homo sapiens
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Warnock DE;
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Gaps

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RESULT 10

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AAR94957 ID AAR9 XX AC AAR9 XX DT 17-P

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(FIVE-) FIVE PRIME THERAPEUTICS INC.
                               2002US-0406579P.
2002US-040658BP.
2002US-040660BP.
2002US-040661BP.
2002US-040661BP.
2002US-040661BP.
2002US-040661BP.
2002US-040664BP.
2002US-040664BP.
2002US-0406655P.
2002US-0406655P.
2002US-0406655P.
2002US-0410946P.
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2002US-0411045P.
2002US-0411046P.
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2002US-0411052P.
2002US-0411055P.
2002US-0411073P.
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2002US-0410953P.
2002US-0410957P.
2002US-0410958P.
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2003US-0463708P.
2003US-0463716P.
2003US-0463732P.
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2003US-0467201P.
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2002US-0410961P.
2002US-0410962P.
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2003US-0471336P.
2003US-0472420P.
  28-AUG-2003; 2003WO-US026780
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2003US-0485224P.
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29-AUG-2002;
29-AUG-2002;
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29-AUG-2002;
29-AUG-2002;
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                                                    89-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                   Drosophila, developmental biology, cell signalling, insecticide, pharmaceutical.
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                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 20796; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.0%; Score 63; DB 4; Length 838; Best Local Similarity 37.1%; Pred. No. 1.9e+02; Matches 13; Conservative 3; Mismatches 15; Indels
                              Drosophila melanogaster polypeptide SEQ ID NO 20796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCRCPCPPSISCNQCPPCAPSTCQCDPIYGFGGKC 528
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                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP29241 standard; protein; 564 AA
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                                                                                                                                                                                                                          PWD,
                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
                                                                                                                                                 23-MAR-2001; 2001WO-US009231
          (first entry)
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                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                   interactions.
          26-MAR-2002
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                                                                                                                           27-SEP-2001
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                                                                                                    New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of apoptase enzymes, designated L100, from the human, mouse and rat. The
                                                                                                                                                                                         The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antifinammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
           Behrens D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding an apoptase, useful e.g. for on treatment of apoptosis-related, especially neurodegenerative,
         Beaurang PA, Behrens D
Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                                                                                   28.8%; Score 62.5; DB 8; Length 564; 39.5%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               3 CNGVCSPFEMPPCGTSACRCIPV---GLVIGYCRNPSG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Lee E, Hestir K, Beaux
3 MM, Kothakota S, Haisha
Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scheek S,
                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                   Claim 1; SEQ ID NO 1239; 428pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BADI ) BASF-LYNX BIOSCIENCE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM51816 standard; protein; 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system injury; stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-2000; 2000DE-01019901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2000; 2000DE-01019901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                           Huang MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kammandel B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine apoptase L100.
Williams LT, Chu A,
Halenbeck RF, Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-649351/75.
                                                                        WPI; 2004-348438/32
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI66273
                                                                                                                                                                                                                                                                                                                                       Sequence 564 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of bracterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment regimes, and identification of compounds useful for the treatment of endometrial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing breast cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant tissue.
protein can be used in the treatment of apoptosis related diseases, including epilepsy, ischaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, multiple sclerosis, central nervous system injury and stroke. The present sequence is the murine apoptase into protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; diagnosis of breast cancer; endometrial cancer; breast tumour; MAI; mitotic activity index; cytostatic.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein LAMB2 differentially expressed in breast cancer tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1798;
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that are differentially expressed in breast cancer tissue
                                                                                                                                                  Length 582;
                                                                                                                                                                                     16; Indels
                                                                                                                                                                                                                                                           239 CDGVCDP-ETCSCSLAGIKCQVMDHTSFPCGCCREGCENPNG 279
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Pred. No. 4.6e+02;
                                                                                                                                                  28.6%; Score 62; DB 4; I 33.3%; Pred. No. 1.7e+02; ive 4; Mismatches 16;
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                                                                                                                                                                                        14; Conservative
                                                                              apoptase L100 protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-180084/23.
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Best Local Similarity
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                                                                                                                                                                       Local Similarity
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                                                                                                                  Sequence 582 AA;
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AAU84346
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7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG
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99US-0123180P.
99US-0125788P.
99US-0125788P.
99US-012664P.
99US-0126785P.
99US-0120714P.
99US-0128714P.
99US-01307449P.
99US-0130845P.
99US-0130845P.
99US-0130845P.
99US-0131848P.
99US-0131848P.
99US-0131848P.
99US-0131848P.
99US-0131848P.
99US-01318218P.
99US-01318221P.
99US-01318221P.
99US-0131823P.
99US-0131823P.
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                                                                                                                                                                                                                                                                                                                            termination sequence
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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01-APR-1999
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                                                                                                                                                                                AAG08039;
                                                                                                            RESULT 16
                                                                                                                              AAG08039
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                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the beta 2 chain of human laminin-15, a novel member of the laminin family that is produced in the retina. The cretina produces 2 novel laminin trimers: laminin-14 (alpha 4, beta 2, gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed within the inter-photoreceptor matrix and in the outer plexiform layer, and may serve to stabilise retinal synapses. The invention provides cand may serve to stabilise retinal synapses. The invention provides laminin-15 preparations and cells comprising a nucleic acid encoding the laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of producing laminin-15. The laminin-15 preparation is used in claimed methods of: increasing retina immunophotoreceptor matrix stability, increasing retina immunophotoreceptor compounds, especially and treating a disorder associated with retinal dependancy increasing retina adhesion; treating a disorder associated with retinal dependancy of synapses of the and retinal detachment; increasing the stability of synapses of the contral nervous system or peripheral nervous system, stability of synapses of the implant, e.g. a catheter, artificial joint, retinal implant, timed conting with the laminin-15 preparation; and increasing photosensitivity by implanting a tip coated with the laminin-15 preparation into an eye. The laminin may be recombinant, and the 3 chains co-expressed in the same
   ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel substantially pure preparation comprising laminin having laminin chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders such as retinitis pigmentosa, macular degeneration, retinal detachment.
   Gaps
 5
                                                                                                                                                                                                                                                                                                      Laminin-15; human; retina; eye; therapy; ophthalmological;
antiinflammatory; rod dystrophy; rod-cone dystrophy;
retinitis pigmentosa; macular degeneration; retinal detachment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cch 28.6%; Score 62; DB 5; Length 1798; al Similarity 36.4%; Pred. No. 4.6e+02; 12; Conservative 4; Mismatches 15; Indels
 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Champliaud M, Hunter D;
                                                       7 CSP--FEMPPCGTSACRCIPVGLVIGYCRNPSG 37
 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The laminin may be recombinant, and (cell or expressed in different cells
                                                                                                                                                              AAM50360 standard; protein; 1798 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MASS-) MASSACHUSETTS GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4A; 58pp; English.
                                                                                                                                                                                                                                                                    Human laminin-15 beta 2 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2001; 2001WO-US013943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000; 2000US-0200863P.
                                                                                                                                                                                                                                 (first entry)
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgeson RE, Brunken W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-041478/05.
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Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI70819.
                                                                                                                                                                                                                                                                                                                                                                                                                WO200183516-A1
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                   18-FEB-2002
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                                                                                                                                                                                               AAM50360;
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Gaps

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 5421.
AAG08039 standard; protein; 94 AA.
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13-AUG-1999;
16-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AU
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05-0CT-1999

06-0CT-1999

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13-0CT-1999

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    8 8
                       990S-0139455P

990S-0139455P

990S-0139455P

990S-0139465P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139750P

990S-014284P

990S-014284P

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990S-014384P

990S-014334P

990S-0144334P

990S-0145918P

990S-014793P

990S-014793P

990S-014793P

990S-014793P

990S-014793P

990S-014793P

990S-014793P

990S-014793P
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23 - 70N - 1999

24 - 70N - 1999

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21-70N-1999;
22-70N-1999;
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23-70N-1999;
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12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
17-AUG-1999;
18-AUG-1999;
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20-AUG-1999;
20-AUG-1999;
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02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
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05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
10-AUG-1999;
                                                                                                                                                                                               - 1999;
                                                                                                                                                                                                                                                                                                                      -JUL-1999;
   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 45884.
                  AAG37331 standard; protein; 94 AA
                                                                                                                                                                                                                                                                                                                                                                        9905-0121825P

9905-0123180P

9905-0125788P

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9905-0128744P

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9905-0134370P

9905-013421P

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99US-0139458P.
99US-0139459P.
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                                                                                        18-OCT-2000 (first entry)
                                                                                                                                                                                                                                Arabidopsis thaliana
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20-MAY-1999;
21-MAY-1999;
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                                                     AAG37331;
AAG3 7331
AAG4 7331
AAG5 7331
AAG6 7331
AAG6 7331
AAG6 7331
AAG7 7
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 Arabidopsis thaliana protein fragment SEQ ID NO: 5420.
                                                                                                                          9905-0121825P.
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9905-012558BP.
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99US-0137524P-
99US-0137724P-
99US-0138640P-
99US-0138847P-
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99US-0139452P-
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99US-0139459P.
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99US-0139763P.
99US-0139817P.
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                                                      Arabidopsis thaliana
                                                                       EP1033405-A2
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21-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG08038 standard; protein; 96 AA
9905-0149902P
9905-0149930P
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9905-0151086P
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Les 15; Conserv
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Best Local S:
Matches 15,
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ID AAG0
XX
AC AAG0
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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9905-0151303P

9905-0151438P

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9905-015559P

9905-015539P

9905-015923P

9905-01609B

9905-016136P

9905-016136P
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Best Local Similarity
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 30 - AUG - 1999;

10 - SEP - 1999;

11 - SEP - 1999;

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15 - SEP - 1999;

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9901S-0139899P

9901S-0140353P

9901S-01406354P

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9901S-0140631P

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7

Gaps

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                                                                                                           16-APR-1999;
19-APR-1999;
                                                                                                                                    21-APR-1999;
23-APR-1999;
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07-MAY-1999;
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   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 3; Length 96;
Pred. No. 46;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 CSPFEMPPCGT----SACRCIPV----GLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :: || | : || || CSPMQLSPCATAITSSSPPSALCCAKLKEQRPCLCGYMRNPS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 5419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG08037 standard; protein; 114 AA
99US-0154039P.
99US-0154039P.
99US-0155486P.
99US-0155486P.
99US-0155486P.
99US-0155486P.
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99US-015923P.
99US-015923P.
99US-015923P.
99US-01609BP.
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ilarity 35.7%;
Conservative 4
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Best Local Similarity
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22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 22-SEP-1999, 23-SEP-1999, 23-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG08037;
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9905-0143542P

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9905-0144332P

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9905-0144333P

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9905-0151065B

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23-AUG-1999;
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26-AUG-1999;
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06-AUG-1999
09-AUG-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.1%; Score 61; DB 3; Length 114;
.larity 35.7%; Pred. No. 53;
Conservative 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 45882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CSPFEMPPCGT----SACRCIPV----GLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSPMQLSPCATAITSSSPPSALCCAKLKEQRPCLCGYMRNPS 90
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2000EP-00301439

25-FEB-2000;

25-FEB-1999

06-SEP-2000

Arabidopsis thaliana

EP1033405-A2.

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APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999 APR-1999	MAX-1999	00-700 00-700 10-70N-1999; 10-70N-1999; 16-70N-1999; 16-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999; 18-70N-1999;	707: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999 708: 1999
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, or the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABOG7826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                        Score 60.5; DB 7; Length 210;
Pred. No. 1e+02;
1; Mismatches 7; Indels 3
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                                                                                                                                                                                                                                                                                                                                  1 ASCNGVCSPFEMPPCGTSACRCIPVG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein SEQ ID #1617.
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                                                                                                                                                                                                                   segdata.uspto.gov/sequence.html
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2002US -0406653P
2002US -0406655P
2002US -0410946P
2002US -0410947P
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2002US-0406608P.
2002US-0406611P.
2002US-0406612P.
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2002US-0410959P.
2002US-0410960P.
2002US-0410961P.
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2002US-0406640P.
2002US-0406642P.
                                                                                                                                                                                                                                                                         Query Match 27.9%;
Best Local Similarity 57.7%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                Sequence 210 AA;
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29-AUG-2002;
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17-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 61; DB 3; Length 114; llarity 35.7%; Pred, No. 53; Conservative 4; Mismatches 11: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSPMQLSPCATAITSSSPPSALCCAKLKEQRPCLCGYMRNPS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CSPFEMPPCGT-----SACRCIPV----GLVIGYCRNPS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 20537; 455pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa polypeptide #3966.
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                                          9905-0159310P

9905-0159631P

9905-0159634P

9905-0160741P

9905-0160741P

9905-0160740P

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9905-0161406P
  99US-0159294P.
99US-0159295P.
99US-0159329P.
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N-PSDB; ABD05362.
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nes 15; Conserv
                                                        14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
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27-JUL-1998;
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Matches
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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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32
ASCNGVCSPFEMPPCGTSACRCIPVGLVIGYC
                                                                                                                                                                                                                       Human secreted protein SEQ ID #1724.
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                                                                                                                    ADP30957 standard; protein; 915
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2002US-0406611P.
2002US-0406612P.
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2002US-0406645P.
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2002US-0410944P.
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2002US-0410948P.
2002US-0410948P.
2002US-0410953P.
2002US-0410953P.
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2002US-0410953P.
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2002US-0410961P.
2002US-0411019P.
2002US-0411022P.
2002US-0411023P.
2002US-0411024P.
2002US-0411034P.
2002US-0411035P.
2002US-0411035P.
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18-APR-2003; 2003US-0463732P
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                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                     RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, encoding a polypeptide which is believed to be cytostatic, antibacterial and virucidal. The composition and methods are useful for diagnosting, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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Haishan L, Linnemann T;
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Halenbeck RF, Huang MM, Kothakota S, 1
Pierce K, Wang Y, Wong JGP, Wu G, Zh
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         17-SEP-2002; 2002US-0411022P.
17-SEP-2002; 2002US-0411023P.
17-SEP-2002; 2002US-0411023P.
17-SEP-2002; 2002US-0411032P.
17-SEP-2002; 2002US-0411032P.
17-SEP-2002; 2002US-0411032P.
17-SEP-2002; 2002US-0411045P.
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17-SEP-2002; 2002US-0411082P.
17-SEP-2002; 2002US-041101P.
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                                                                                                                                                                                                                                                      17-SEP-2002; 2002US-0411101P.
18-APR-2003; 2002US-0411111P.
18-APR-2003; 2003US-0463708P.
18-APR-2003; 2003US-0463708P.
18-APR-2003; 2003US-0463716P.
18-APR-2003; 2003US-0463716P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467201P.
19-MAY-2003; 2003US-047306P.
19-MAY-2003; 2003US-047306P.
22-MAY-2003; 2003US-047306P.
22-MAY-2003; 2003US-0476609P.
09-JUN-2003; 2003US-0476609P.
09-JUN-2003; 2003US-0476609P.
08-JUL-2003; 2003US-0476609P.
08-JUL-2003; 2003US-0476609P.
08-JUL-2003; 2003US-0476609P.
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2002US-0410961P.
2002US-0410962P.
2002US-0411019P.
2002US-0411022P.
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2002US-0411037P.
2002US-0411041P.
2002US-0411045P.
2002US-0411046P.
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2002US-0411073P.
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2002US-0411111P.
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2003US-0463700P.
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2003US-0463732P.
2003US-0467199P.
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2003US-0467233P.
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2003US-0472420P.
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2003US-0476641P.
2003US-0485218P.
2003US-0485218P.
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2002US-0411052P
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2003US-0493573P.
2003US-0493577P.
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17-SEP-2002;
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                     29-APR-2004
     New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haishan L,
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Halenbeck RF, Huang MM, Kothakota S, Hais
Pierce K, Wang Y, Wong JGP, Wu G, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2955; 428pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      (FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein SEQ ID #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP29284 standard; protein; 576
                                                                                                                                                                                         2003US-0485223P
2003US-0485224P
2003US-0486446P
2003US-0486480P
2003US-0486480P
2003US-048690P
2003US-048691P
2003US-0493341P
2003US-0493341P
                                                                   2003US-0471306P.
2003US-0471336P.
2003US-0472420P.
                                                                                                                      2003US-0472430P.
2003US-0476609P.
2003US-0476641P.
2003US-0485218P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-348438/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 915 AA;
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02-MAY-2003; 202-MAY-2003; 202-MAY-2003; 202-MAY-2003; 202-MAY-2003; 222-MAY-2003; 222-MAY-2003; 222-MAY-2003; 209-UUL-2003; 209-UUL-2003; 209-UUL-2003; 209-UUL-2003; 214-UUL-2003; 214-UUL-2003; 215-UUL-2003; 215-UUL-2003; 209-AUG-2003; 209
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antibated antinflammatory, immunosuppressive, antibaterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence as a number of the second sequence is available on WIPOWEB and is not in the specification.
                                                              Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1282; 428pp; English.
                     (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                             WPI; 2004-348438/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 576 AA;
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1; Gaps Query Match 27.4%; Score 59.5; DB 8; Length 576; Best Local Similarity 50.0%; Pred. No. 3.2e+02; Matches 12; Conservative 2; Mismatches 9; Indels 1 15 CGTSACR-CIPVGLVIGYCRNPSG 37 ઠે

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Search completed: March 28, 2005, 08:57:08 Job time : 97 secs

108 GGIKSCRGFLDQGLDDNYCRNPDG 131

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Q6alc6 bituminaria Q6alc1 onobrychis Q6alc5 caragana ar Q7qs94 giardia lam Q8ihd9 drosophila	Q8ml84 drosophila P5331 homo sapien Q9y5w5 homo sapien Q6uxil homo sapien Q76952 aedes aegyp	099kr2 mus musculu 0924y6 rattus norv 09wual mus musculu 06in38 rattus norv 019137 mus musculu	Q7qt99 giardia lam Q6dj29 xenopus tro P27606 chlamydia p Q7psp7 anopheles g	P90769 caenorhabdi Q7r5j3 giardia lam Q69za9 mus musculu Q66gr4 rattus norv Q6pze0 mus musculu	P94663 chlamydophi Q8h0y6 arabidopsis Q817g7 arabidopsis Q942d3 oryza sativ	Qsebal navoluce ca Qsais8 chlamydophi Q72bj2 desulfovibr P49705 gallus gall	O/rawl plasmodium Q6ifwl rattus norv Q9pzr6 human cytom O97887 bos taurus		Qespina coe carrie Q86yu6 homo sapien Q66t09 brachydanio Q6w4t8 brachydanio	Q911Ke araulogese Q8t0ws pimpla Q9bee3 macaca fasc Q9nb50 riftia pach	decp14 Kluyveromyc P51971 saccharomyc P67983 bos taurus P67982 ovis aries	P095/7 Ovis aries P09578 ovis aries Q8mii4 bos taurus Q667522 bos mutus g	Q6/zwo aspergillus Q9mg37 caenorhabdi Q9y6n6 homo aspien Q8mg36 caenorhabdi O67w49 croya asriv	Q9xzyl leishmania Q9xzyl leishmania O1828s caenorhabdi Q9w6f8 xenopus lae Q79s28 anopheles g	
83 37.4 59 2 80 36.0 60 2 72 32.4 58 2 64 28.8 536 2	539 2 3075 1 379 1 1847 2	60.5 27.3 220 2 60.5 27.3 365 2 60.5 27.3 379 1 60.5 27.3 379 2	58.5 26.4 592 2 07079 58 26.1 494 2 06DJ2 57.5 25.9 421 2 07P8P	25.9 440 2 25.9 574 2 25.9 618 2 25.9 3550 2 25.9 7524 2	57 25.7 88 2 57 25.7 91 2 57 25.7 92 2 57 25.7 636 2	57 25.7 722 I 56.5 25.5 87 2 56.5 25.5 371 2 56 25.2 311 1	55 25:2 404 55.5 25:0 404 55.5 25:0 175	55.5 25.0 461 1 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 25.0 1637 2 55.5 2 55.0 1637 2 55.5 2 55.0 1637 2 55.5 2 55.0 1637 2 55.5 2 55.0 1637 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5 2 55.5	55 24.8 264 55 24.8 264 55 24.8 264	54.5 24.5 191 2	54.5 24.5 921 2 54.5 24.5 965 1 54 24.3 61 1 54 24.3 61 1	54 24.3 54 24.3 54 24.3 54 24.3 61 1	54 24.3 819 2 54 24.3 1299 2 54 24.3 1587 1 54 24.3 2427 2	53.5 24.1 277 53.5 24.1 371 53.5 24.1 374 53.5 24.1 1859	53 23.9 119 2 53 23.9 119 2 53 23.9 140 2
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - protein search, using sw model Run on: March 28, 2005, 08:40:49; Search time 84 Seconds (without alignments) 225.559 Million cell updates/sec	Title: US-09-674-496D-8 Perfect score: 222 Sequence: 1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGPCIHPTG 37	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1612378 segs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	Database : Uniprot_03:* 1: uniprot_sprot:* 2: uniprot_trembl:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES  Query	222 100.0 119 1 ALB1 SOYBN Q39837 216 97.3 119 1 ALB1 GLYSO Q92GX0	108 93.7 100 2 Q.YAZG3 109 86.5 89 1 ALABU QQFTCB 169 76.1 96 2 Q6AIC7 168 75.7 140 2 Q.YAZG5 QGAIC7	7 165 74.3 130 1 ALIB PEA . P62927 $962927$ $96107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$ $963107$	1 161 72.5 130 1 ALID PEA 2 158 71.2 98 2 Q6AIC9 3 158 71.2 130 1 ALIE PEA 4 155 69.8 130 1 ALIA PEA	55 154 69.4 99 2 QAAIC8 Q6AZCB C	1 137.5 61.9 101 2 06A103 06A103 06A103 06A103 0 101 2 06A103 0 06A103 0 06A104	121 54 109 499 103 46 88 399 83 37

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Length 119;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tan J.Z., Lou C.F., Hirano H.;
Wild species (Glycine soja).";
Chin. J. Appl. Environ. Biol. 5:259-263(1999).
-!- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its phosphorylation activity (By similarity).
-!- PTM: The C-terminal glycine may be removed from Alb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 46, Last Sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 precursor (A1) [Contains: Albumin 1 chain b (A1b)
[Leginsulin]; Albumin 1 chain a (Ala)].
Glycine soja (Wild soybean).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I: Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
R->A: No effect.
V->A: Decreased binding to globulin.
F->A: Decreased binding to globulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Albumin 1 chain b (By similarity).
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Albumin 1 chain a (Potential).
Potential.
By similarity.
By similarity.
By similarity.
                                                                                                         13046 MW; A054491D7BE1AA70 CRC64;
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EE5457D8D09070CC CRC64;
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                                                                                                                                              Score 222; Db -, No. 2.3e-20;
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Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                              20 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG
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                                                                                                                                                                                                            100.0%; Pred. No. 2.3 ive 0; Mismatches
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01-OCT-2003 (TrEMBLrel. 25, Created)
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                                                                                                      SEQUENCE
                                                                                                                                                                               Query Match
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Matches
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Q7XZC3
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                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine. NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 270:1269-1276(2003).
-1- FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 20-56, MUTAGENESIS OF ARG-35; VAL-48 AND PHE-50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12631285;
Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K.,
Nishiuchi Y., Hirano H.;
"A possible physiological function and the tertiary structure of a kDa peptide in legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. Miyagishirome; TISSUE=Radicle;
MEDIAINE=94357216; Pubmed=8076638;
Watanabe Y., Barbashov S.F., Komatsu S., Hemmings A.M., Miyagi M., Tsunasawa S., Hirano H.;
"A peptide that setimulates phosphorylation of the plant insulinbinding protein. Isolation, primary structure and cDNA cloning.";
Eur. J. Blochem. 224:167-172(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Miyagishirome,
Tran J.Z., Lou C.F., Hirano H.;
"Analysis of leginsulin gene in soybean cultivar (Glycine max) and
wild species (Glycine soja).";
Chin. J. Appl. Environ. Biol. 5:259-263(1999).
                                                                                                         ALD: SOLING (199884).
16-OCT-2001 (Rel. 40, Created).
16-OCT-2001 (Rel. 40, Last sequence update).
15-OCT-2004 (Rel. 45, Last annotation update).
25-OCT-2004 (Rel. 45, Last annotation update).
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Potential.
Albumin 1 chain a (Potential)
Potential.
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                                                                                                                                                                                                                                                                       Albumin 1 precursor (A1) [Contains: Albi
(Leginsulin); Albumin 1 chain a (A1a)].
Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirano H.; Submitted (JUN-2001) to Swiss-Prot.
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### SABL; D17396; BAA.

### SAB192; S48192.

### SAB193; S48192.

#### SAB193; S48193; S481
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                                                                                                      STANDARD;
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REVISION TO 64.
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Hirano H

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Gaps

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Length 119;

us-09-674-496d-8.rup

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SEQUENCE
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Matches
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Q6A1C7
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-I- FUNCTION: Alb binds to basic 75 globulin (BG) and stimulates its phosphorylation activity (By similarity).
-I- PTM: The C-terminal glycine may be removed from Alb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phaseolus aureus (Mung bean) (Vigna radiata).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Pabacese; Papilionoidese; Phaseolese; Vigna.
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                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,

Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,

Molacular A., Rahbe Y.;

Molacular and biological screening for insect-toxic seed albumins

from four legume species.",

Plant Sci. 167:705-714(2004).

Plant Sci. 167:705-714(2004).

EMBL, AJ574791; CAE00463.1; -.

Signal.

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25-OCT-2004 (Rel. 45, Last annotation update)
Albumin 1 precursor (A1) [Contains: Albumin 1 chain b (A1b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AA; 10982 MW; 281D9CE0F8E83611 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Albumin 1 precursor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 208; DB 2;
Pred. No. 1.1e-18;
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Plant toxin; Seed storage protein; Signal.
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SEQUENCE FROM N.A.
STRAIN=CV. Blackmappe; TISSUE=Leaf;
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91.9%;
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56
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PubMed=12631285;
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Q9FRT8;
                                                                                       Name=pal;
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SEQUENCE
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                                                                                                                                                                                                                                                            Gaps
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol.O.,
Chessel D., Rahbe Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosićeurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Vicia.
                                 Albumin 1 chain b (By similarity).
Potential.
Albumin 1 chain a (Potential).
By similarity.
By similarity.
By similarity.
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Last annotation update)
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Last annotation update)
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putative albumin 1b.
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larity 67.6%; Pred. No. 9.3e-14;
Conservative 7; Mismatches 5;
                                                                                                                                                                                                                    Score 192; DB 1;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                             96 A.A.
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                                                                                                                                                                                                                                                            3; Mismatches
                    Potential.
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25-0CT-2004 (TrEMBLrel. 28, Last sequen
25-0CT-2004 (TrEMBLrel. 28, Last annota
Putative albumin 1 precursor (Fragment)
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27 63 pu
69 >96 pu
96 96 mw, I
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>89
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9711 MW;
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Best Local Similarity 83.8%;
Matches 31; Conservative
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Q7XZC5;
01-0CT-2003 (TrEMBLrel. 2:
01-0CT-2003 (TrEMBLrel. 2:
01-0CT-2003 (TrEMBLrel. 2:
Albumin 1 precursor.
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SEQUENCE
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DISULFID
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PROPEP
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SIGNAL
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                                                                                                                                                              CHAIN
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Q6A1D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Higgins T.C. V., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis of an allur-rich protein in pea seeds."; Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: Increasing expression during seed development followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Birte; TISSUB=Cotyledon;
Domonov C., Blis N., Welham T.;
"Genetic loci controlling albumin synthesis in Pisum.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PAID binds to basic 75 globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide. Toxic to various insects through binding to a high
affinity binding site in the insect the Similarity.
-!- TISSUE SPECIFICITY: Major comopnent of both the cotyledons and
                                                                                                                                                                                                                                                                                                 Gaps
                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                             P62927; P08687; Q40999; Q9M3X4; O1-JAN-1988 (Rel. 06, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Albumin 1 B precursor (PAL B) (Contains: Albumin 1 B chain b (PAlb Pisum sativum (Garden pea).
                                                                                         SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rahbe Y.,
"Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY STRAIN-cv. Greenfeast; TISSUE-Seed; MEDLINE-86278210; PubMed-3755437;
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0
                                                                                                                                                                                                                                                                    Score 168; DB 2; Length 140;
Pred. No. 1.8e-13;
6; Mismatches 4; Indels
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519D9CEAB8924855 CRC64;
                                                                                                                                                                                                                                                                                                                                       29 DCSGACSPFEMPPCRSSDCRCIPIGLVAGYCTYPS 63
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                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA.
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               Medicago truncatula (Barrel medic)
                                                                                                                                              from four legume species.";
Plant Sci. 167:705-714(2004).
EMBL, AJ574789; CAE00461.1; --
HSSP; Q39837; lJUB
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28 140 a
140 AA; 15426 MW;
                                                                                                                                                                                                                                                                     75.7%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                 NCBI_TaxID=3880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3888;
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AL1B PEA
ID AL1B PEA
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SIGNAL
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                loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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as its content is in no
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Galegeae, Astragalus.
NCBI_TaxID=287756;
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,

Chessel D., Rahbe Y.,
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                                                                                                                                                                                                                                                                                                                                                                                               Score 165; DB 1; Length Lister Pred, No. 3.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Broad screening of the legume family for variability of activities and occurence of seed albumin 1b toxins."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                              F8B134A334490F5F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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Pred. No. 5.6e-13;
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                                                                                                                                                                                        Albumin 1 B chain b. Potential.
Albumin 1 B chain a. Potential.
By similarity.
By similarity.
By similarity.
M -> I (in Ref. 2).
Q -> P (in Ref. 2).
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putative albumin 1a
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              modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AA
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                                                                                           EMBL, M13790, AAA33639.1; -.
EMBL, AJA76863, CAR82695.1; -.
InterPro, IPRO11036; PH related.
Plant toxin, Seed storage protein; Signal.
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64 63
70 122
73 130
7 46
8 48
58 10 M
120 O
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74.3%;
Best Local Similarity 67.6%;
Matches 25; Conservative
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eurosids I; Fabales; Fabaceae; Papilionoideae; Desmodieae;
                    NCBI_TaxID=287750;
                                            SEQUENCE FROM N.A
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             Alysicarpus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                                                                                                                                                                                           Yamazaki T., Takaoka M., Katoh E., Hanada K., Sakita M., Sakata K., Nishiuchi Y., Hirano H.; "A possible physiological function and the tertiary structure of a 4-KDa peptide in legumes."; Eur. J. Biochem. 270:1269-1276(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                 Bukaryota, Viridiplantae, Streptophytä, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Vigna.
                                                                                                                                                                                                                                                                                                     FUNCTION: Alb binds to basic 7S globulin (BG) and stimulates its phosphorylation activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                             , Last sequence update)
, Last annotation update)
(Al) [Contains: Albumin 1 chain b (Alb)
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                                                                                                                                       Phaseolus angularis (Adzuki bean) (Vigna angularis)
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Last annotation update)
                                                                                                     Albumin 1 precursor (A1) [Contains: Albumin 1 chair (Leginsulin); Albumin 1 chain a (A1a)] (Fragment).
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Pred. No. 7.8e-13;
6; Mismatches 5
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similarity.
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HSSP, Q39837; 1JU8.
Plant toxin; Seed storage protein; Signal.
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Potential.
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                                                                                                                                                                                                                    STRAIN=cv. Dainagonazuki; TISSUE=Leaf;
PubMed=12631285;
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26; Conservative
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                                              STANDARD;
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                                                                               (Rel. 40, (Rel. 45,
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                                                                                                                                                                                     NCBI_TaxID=3914;
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Q9FRT9;
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0661D6
DG 0661D
AC 0661D
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DT 25-0C
DE Putat
GN Name=
GN SPERT
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MEDLINE=8678210; PubMed=3755437;
Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Higgins T.J.V., Chandler P.M., Inglis A.S.;
Higgins T.J.V., Chandler P.M., Inglis A.S.;
Higgins Extructure, protein in pea seeds.";
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
-1-FUNCTION: Palb binds to basic 78 globulin (BG) and stimulates its
phosphorylation activity. Involved in the signal transduction
system to regulate the growth and differentiation as a hormone
peptide. Toxic to various insects through binding to a high
affinity binding site in the insect gut (By similarity).

Hissue Specific Try: Major comopnent of both the cotyledons and
embryonic axes of mature seeds.

-1- DEVELOPMENTAL STAGE: Increasing expression during seed development
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                                                                                                                                                                                                                                                                                                                  SECURNCE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.,
Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis a sulfur-rich protein in pea seeds."; J. Biol. Chem. 261:11124-11130(1986).
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Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 161; DB 2; Lengtn 91., Pred. No. 9.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB9B9278F3EF5B06 CRC64;
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Plant Sci. 167:705-714(2004).
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>91
91
9890 MW;
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Best Local Similarity 73.0%;
Matches 27; Conservative
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Signal.
SIGNAL 18
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Length 98;

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1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
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Best Local Similarity
Matches 23; Conserv
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PubMed=9749674
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Higgins T.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Hedysareae; Onobrychis.
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;

"Broad screening of the legume family for variability of insecticidal
                                       PTM: The C-terminal glycine may be removed from PAlb. MISCELLANBOUS: The protein sequenced in Ref.2 was probably a mixture of the products of genes C and D, PAlb being of C origin while PAla is of D origin.
                                                                                                                                                                                                                                                                                                                                         Direct protein sequencing, Plant toxin, Seed storage protein, Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
followed by a rapid degradation during the first days of seed germination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 161; DB 1; Length 130;
.larity 62.2%; Pred. No. 1.3e-12;
Conservative 8; Mismatches 6; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AJ784949; CAH05249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ' similarity.
823AA340ACD9535C CRC64;
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63 putative albumin lb.
98 putative albumin la.
10830 MW; 03072C77178AIE83 CRC64;
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Last annotation update)
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By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                    EMBL; AJS74794; CAE00466.1; -.
InterPro; IPR011036; PH_related.
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130 AA;
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les 23; Conserv
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Q6A1C9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIE PEA STANDARD; PRT; 130 AA.
P62930; P08687; Q40999; Q7XZC1; Q9M3X4;
D1-JAN-1988 (Rel. 06, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
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25-OCT-2004 (Rel. 45, Last annotation update)
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Plant Sci. 167:705-714(2004).
-!-FUNCTION: PAID binds to basic 7S globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide. Toxic to various insects through binding to a high affinity binding site in the insect gut (By similarity).
-!- PTM: The C-terminal glycine may be removed from PAID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morton R.L., Ellery A.J., Higgins T.J.; "Downstream elements from the pea albumin 1 gene confer sulfur responsiveness on a reporter gene."; Mol. Genet. 259:309-316(1998)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rahbe Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 158; DB 1; Length 130;
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71.2%; Score 158; DB 2; L
76.5%; Pred. No. 2.3e-12;
Minmatches 5;
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Potential.
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EMBL; AJ574795; CAE00467.1; -.
InterPro; IPR011036; PH related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 A A 69 B D 122 A. 130 P P 46 B B 13778 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%;
                                                                                  Local Similarity 76.5
nes 26; Conservative
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PG2931; P08687; Q40999; Q7X9N3; Q9M3X4; 01-JAN-1988 (Rel. 06, Created) 25-OCT-2004 (Rel. 45, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Albumin 1 F precursor (PA1 F) (PsaAlbOO5/PsaAlbO11) [Contains: Albumin 1 F chain b (PA1b F) (Leginsulin F); Albumin 1 F chain a (PA1a F)].
                                                                                                                                                                                                                                                                                                                                                                                                                 Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis of a sulfur rich protein in pea seeds."; J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                           Trigonelia foenum-graecum (Fenugreek).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Spermatophyta, Magnoliophyta, Papitostyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaces, Papitlionoideae, Trifolieae, Trigonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Broad screening of the legume family for variability of insecticidal activities and occurrence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ784950; CAH05250.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pisum sativum (Garden pea).

Bukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euvrosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vallier A., Rahbe Y.; ^{*} Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol
Chessel D., Rahbe Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Delobel B., Grenier A., Gueguen J., Ferrasson E., Mbailao M.;
"The of a polypeptide derived from a PAlb legume albumen as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Frisson; TISSUE=Seed;
Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94D20EAD462018B4 CRC64;
                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.4%; Score 154; DB 2; L
70.6%; Pred. No. 7.6e-12;
iive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative albumin 1b. putative albumin 1a.
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                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequen
25-OCT-2004 (TrEMBLrel. 28, Last annots
Putative albumin 1 precursor (Fragment)
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STRAIN=cv. Frisson; TISSUE=Seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 27 PC
28 64 pu
72 >99 pu
99 99 AA; 10783 MW; 5
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Plant Sci. 167:705-714(2004).
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=78534;
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
STRANS=CV. Greenfeast; TISSUE-Seed;
MEDLINE=86278210; PubMed=3755437;
A MEDLINE=86278210; PubMed=3755437;
A Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
A Blagrove R.J., Kortt A.A., Inglis A.S.;
T "Gene structure, protein in pea seeds.";
J. Blol. Chem. 261:11124-11130(1986).
I. Blol. Chem. 261:11124-11130(1986).
C -! FUNCTION: PALD binds to basic 78 globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide. Toxic to various insects through binding to a high affinity binding site in the insect gut (By similarity).
C -! TISSUE SPECIFICITY: Major comopnent of both the cotyledons and embryonic axes of mature seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute of There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib>eib.ch).
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                                                                                                                                                                                           ALIA PEA PEA STANDARD; PRT; 130 AA. P66256; P08687; Q40999; Q9M3X4; D1-JAN-1988 (Rel. 06, Created) O1-JAN-1988 (Rel. 06, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Albumin 1 A precursor (PAI A) [Contains: Albumin 1 A chain b (PAIb A) Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
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Pred. No. 7.2e-12;
7; Mismatches 7; Indels
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1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
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Albumin 1 A chain
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Best Local Similarity
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Gaps

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STRUCTURE BY NMR OF 27-63, AND DISULFIDE BONDS PubMed=14556622; DOI=10.1021/bi0348031;

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Length 98;

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Chessel D., Ranbe Y.;
"Broad screening of the legume family for variability of insecticidal activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;
Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784943; CAH05243.1;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Psoraleeae,
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Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R.,
Blagrove R.J., Kortt A.A., Inglis A.S.;
Gene structure, protein structure, and regulation of the synthesis
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
   SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Louis S., Delobel B.,
Chessel D., Rahbe Y.,
Chessel D., Chessel D.,
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Pred. No. 1.3e-11;
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Pred. No. 1.8e-11;
3; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Ing as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                              Gressent F., Rahioui I., Rahbe Y.;

"Characterization of a high-affinity binding site for the pea albumin "Characterization of a high-affinity binding site for the pea albumin be entomotoxin in the weevil Sitophilus";

Bur. J. Biochem. 270:2429-2435(2003).

-I. FUNCTION: PALD binds to basic 7S globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide (By similarity). Toxic to various insects through binding to a high affinity binding site in the insect gut.

-I. PTM: The C-terminal glycine may be removed from PAlb.

-I. PTM: PAlb displays a cysteine-knot (knottin) fold.
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Jouvensal L., Quillien L., Ferrasson E., Rahbe Y., Gueguen J.,
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PDB, 1P8B, NMR; A=27-63.
InterPro; IPR011036; PH_related.
3D-structure; Direct protein sequencing; Plant toxin;
                                       Vovelle F.;
Palb, an insecticidal protein extracted from pea see
sativum:: 1H-2-D NMR study and molecular modeling.";
Biochemistry 42:11915-11923 (2003).
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Gaps

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Indels

62

Length 99;

Length 101;

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Query Match
Best Local Similarity
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PROPEP
                 Best Loc
Matches
                                                                                                                                                       ALIC_PEA
                                                                                                                                       RESULT
                                                                                        원
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.,
"Broad screening of the legume family for variability of insecticidal
                                                                                       Phaseclus vulgaris (Kidney bean) (French bean).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabacese; Papilionoidese; Phaseolese
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Higgins T.J., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.; "Gene structure, protein structure, and regulation of the synthesis a sulfur-rich protein in pea seeds."; a sulfur-rich protein in pea seeds."; J. Biol. Chem. 261:11124-11130(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lonchocarpus capassa (Apple-leaf).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
euroaida I; Rabales; Rabaceae; Papilionoideae; Millettiaee;
                                                                                                                                                                                                                              Molecular and biological screening for insect-toxic seed albumins
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Quillien
Valiter A., Rahbe Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ784945; CAH05245.1; -.
                                                                                                                                                                                                                                                                                                                            1 27 Potential.
28 65 Alb, albumin lb.
74 >109 Ala, albumin la.
109 AA; 11923 MW, E420417E90D35IAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0B8A138465E7C19B CRC64;
            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative albumin lb. putative albumin la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CNGACSPEEVPPCRS-RDCRCVPIGLFVGFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                     66.9%; Score 148.5; DB 2, 66.7%; Pred. No. 4.1e-11; tive 5; Mismatches 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative albumin 1 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                           from four legume species.";
Plant Sci. 167:705-714(2004).
EMBL; AJ574722; CAE00464.1; -.
HSSP; Q39837; LJU8.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 25 Pot
26 65 put
74 ×101 put
101 101
101 AA; 11003 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 66.7%;
les 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3926;
                                                                                                                                                    NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=pal;
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SEQUENCE
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SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                 ALIC PEA STANDARD; PRT; 130 AA.
P62928; P08687; Q40999; G7XZC0; Q9M3X4;
P62928; P08687; Q40999; Greated)
D1-JAN-1988 (Rel. 06, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
26-OCT-2004 (Rel. 45, Last annotation update)
27-OCT-2004 (Rel. 45, Last annotation update)
28-OCT-2004 (Rel. 45, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Higgins T.J.V., Chandler P.M., Randall P.J., Spencer D., Beach L.R., Blagrove R.J., Kortt A.A., Inglis A.S.;
Blagrove R.J., Kortt A.A., Inglis A.S.;
"Gene structure, protein structure, and regulation of the synthesis of a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
-- FUNCTION: PAID binds to basic 78 globulin (BG) and stimulates its phosphorylation activity. Involved in the signal transduction system to regulate the growth and differentiation as a hormone peptide. Toxic to various insects through binding to a high affinity binding site in the insect gut (By similarity).
-- TISSUE SPECIFICITY: Major component of both the cotyledons and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryonic axes of mature seeds.
-!- DEVELOPMENTAL STAGE: Increasing expression during seed development followed by a rapid degradation during the first days of seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- PTM: The C-terminal glycine may be removed from PAlb.
-I- MISCELLANEOUS: The protein sequenced in Ref.2 was probably a mixture of the products of genes C and D, PAlb being of C origin while PAla is of D origin.
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. Frisson; TISSUB=Seed;
Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rahbe Y.;
Molecular and biological screening for insect-toxic seed albumins
from four legume species.";
Plant Sci. 167:705-714(2004).
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                                                           Indels
                                                                                                                   37
                                                                                                                                                                           65
                                                                                                                                                  26 ASCNGRDVCSPFEMPPCDDATNCRCIPWGLVVGQCVHPSG
                                                                                                                   1 ADCNG--ACSPFEVPPC-RSRDCRCVPIGLFVGFCIHPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albumin 1 C chain b.
Score 137.5; DB 2
Pred. No. 9.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
By similarity.
By similarity.
                                                           6; Mismatches
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or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=86278210; PubMed=3755437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ574796; CAE00468.1; -.
InterPro; IPR011036; PH related.
Direct protein sequencing; Plant
SIGNAL
61.9%;
60.0%;
                                                        24; Conservative
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63
69
122
130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
PROPEP
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Similarity
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SEQUENCE
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Q6A1D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Louis S., Delobel Y.,
"Rahbe Y.,
"Broad screening of the legume family for variability of insecticidal
activities and occurence of seed albumin 1b toxins.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ784946; CAHO5246.1; -.
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae, Melilotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lupinus angustifolius (Narrow-leaved blue lupine).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eddicotyledons, core endicots, rosids,
eurosids I; Fabales, Fabaceae, Papillonoideae, Genisteae, Lupinus.
NCBI_TaxID=3871;
                                                                                                                        ö
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                                                                              61.3%; Score 136; DB 1; Length 130; 60.0%; Pred. No. 1.8e-09; ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-0CT-2004 (Rel. 45, Last annotation update)
Albumin 1 precursor (Al) (Contains: Albumin 1 chain b (Alb)
(Leginsulin); Albumin 1 chain a (Ala)] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128; DB 2; Length 98;
Pred. No. 1.4e-08;
7; Mismatches 9; Indels
By similarity.
N -> H (in Ref. 2).
12C8EA2B8300A723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 Potential.
63 putative albumin lb.
>98 putative albumin la.
98
10691 MW, EF28472D8D9498AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                             CNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
                                                                                                                                                                                    29 CNGVCSPFDIPPCGSPLCRCIPAGLVIGNCRNPYG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPT 36
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                                                                                                                                                                                                                                                                                                      98 AA
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                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Last sequen
25-OCT-2004 (TrEMBLrel. 28, Last annota
Putative albumin 1 precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Melilotus alba (White sweet clover)
                                                                                                                                                                                                                                                                                                      PRT;
  41 58 By
60 60 N
130 AA; 13912 MW;
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llarity 54.3%;
Conservative
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                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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les 19; Conserv
                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=47082
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DISULFID
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                          RESULT 22 . 106A1D2 AC Q6A1D2 AC Q6A1D2 DT 25-OC DT 25-OC
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Matches
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Blagrove R.J., Kortt A.A., Inglis A.S.;
Gene structure, protein structure, and regulation of the synthesis of
a sulfur-rich protein in pea seeds.";
J. Biol. Chem. 261:11124-11130(1986).
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                                                                                                                                                                 Flant Mol. Biol. 34:613-627(1997).
-!- FUNCTION: Alb binds to basic 78 globulin (BG) and stimulates its phosphorylation activity (By similarity).
-!- PTM: Three disulfide bonds are probably present.
-!- PTM: The C-terminal glycine may be removed from Alb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Louis S., Delobel B., Gressent F., Rahioui I., Duport G., Diol O.,
Chessel D., Rahbe Y.;
SEQUENCE FROM N.A.
STRAIN=cv. Unicrop;
MEDLINE=97390686; PubMed=9247543; DOI=10.1023/A:1005868105651;
Ilgoutz S.C., Knittel N., Lin J.M., Sterle S., Gayler K.R.;
"Transcription of genes for conglutin gamma and a leginsulin-like protein in narrow-leafed lupin.";
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Albumin 1 chain a (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70014D8E9BBF5439 CRC64;
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Last annotation update)
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putative albumin 1b.
putative albumin 1a.
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Pred. No. 2.9e-08;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
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Plant toxin; Seed storage protein.
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80.8%;
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
NCBI_TaxID=3880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Louis S., Delobel B., Gressent F., Rahioui I., Quillien L.,
Vallier A., Rabbe Y.;
Vallier A., Rabbe Y.;
Wolledular and biological screening for insect-toxic seed albumins
from four legume species.";
Plant Sci. 167:705-714(2004).

EMBL, A5574999; CASE00462.1; -.

HSSP; Q39837; 1JU8.
                                                                                                                                                                                                  3;
                                                                                                           Query Match 56.1%; Score 124.5; DB 2; Length 101; Best Local Similarity 55.3%; Pred. No. 4.1e-08; Matches 21; Conservative 8; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.3%; Pred. No. 1.6e-07;
Matches 19; Conservative 6; Mismatches 10; Indels
101 101
101 AA; 11068 MW; 26ECD6B970BD10E2 CRC64;
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CHAIN 28 142 albumin 1.
SEQUENCE 142 AA; 15727 MW; F35A1A5A9EDA9E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7XZC4;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Albumin 1 precursor.
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SEQUENCE
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      GenCore version 5.1.6
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A; Rosidues: 1-3075 - HAA>
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A; Rosiennen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A; Rittle: Primary structure of the human laminin A chain. Limited expression in human tiss
A; Reference number: S14663; MUID:91264789; PMID:2049067
A; Reference number: S14663
A; Rolocule type: mRNA
A; Residues: 1-227, FEC, 230-251, MLP, 255-418, EC, 420-518, LC, 520-1022, VC, 1024-1074, VC, JJ
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A; Clsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki, JL
Lab. Invest. 60, 772-782, 1989
A; Pittle: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 chail
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y,Cross-references: GDB:120135; OMIM:150320
y,Cross-references: GDB:120135; OMIM:150320
y,Cross-references: GDB:12013-18p11.22
y,Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hcl; Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide boncl; fila)77Domain: signal sequence #status predicted <SIG>y,1-17/Domain: signal sequence #status predicted <SIG>y,1-17/Domain: V <DOM6>
y,18-269/Domain: V <DOM6>
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F;2229-2484/Domain: laminin G repeat homology <LG3>
F;2214-2556/Founain: laminin G repeat homology <LG3>
F;2514-2556/Region: cell attachment (R.-G-D) motif
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F;2916-3073/Domain: laminin G repeat homology <LG5>
F;381,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,18
rate (ABR) (covalent) #status predicted
F;297-305/Disulfide bonds: #status predicted
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F;277-461/Domain: laminin-type EGF-like homology <LE3>
F;261-512/Domain: laminin-type EGF-like homology <LE4>
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A,Reference number: S14458; MUID:91333420; PMID:1714537
A,Accession: S14458
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A;NOte: the authors translated the codon AGA for residue 2692 as Pro
C;Genetics:
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                                                                                                                                                   A, Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12126-3075/Domain: G < DOMG>
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A34961
                                                                                                                                                                                                                                  figulin-like growth factor S11 precursor - soybean
NiAlternate names: leginsulin
() Species: Olycine max (soybean)
() Species: Decession: S48192; PN016
() Accession: S48192; PN016
() Aritle: A peptide that stimulates phosphorylation of the plant insulin-binding protein.
A) Airlie: A peptide that stimulates phosphorylation of the plant insulin-binding protein.
A) Molecule type: mRNA; protein
A) Molecule type: mRNA; protein
A) Residues: 1-119 < WATP.
A) Residues: NONIPROT: O39837; GB: D17396; NID: G498167; PIDN: BAA04219.1; PID: G498168
A) Reference number: PN0115; MUID: 91066897; PMID: 2250683
A) Reference number: PN0115; MUID: 91066897; PMID: 2250683
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C;Genetics:
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C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S14458; S14663; A34961
R;Haaparanca, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: PN0116
A;Molecule type: protein
A;Residues: 20-30,'W',32-39 <BAR>
F;1-19/Domain: propeptide #status predicted <PRO>
F;20-56/Product: insulin-like growth factor S11 #status experimental <MAT>
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62.2%; Pred. No. 1.3e-11;
tive 7; Mismatches 7; Indels
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F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-130/Product: albumin #status predicted <MAT>
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              ALIGNMENTS
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S14458
laminin alpha-1 chain precursor - human
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Matches 37; Conservative
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A; Molecule type: mRNA
A; Residues: 1-3084 <SAS>
A; Cross-references: UNIPROT: P19137; EMBL: J04064; NID: g309419; PIDN: AAA39410.1; PID: g3094;
A; Accession: A30449
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 183-195; 570-571, 'A', 573-586, 596-612, 'X', 614-617, 'EMK'; 630-646; 1217-1222, 'YPF
2486; 2624-2639; 2818-2843; 3009-3033, 'V', 3035 <SA2>
R; Hartl, L.; Oberbaeumer, I.; Deutzmann, R.
Bur. J. Blochem: 173, 629-635, 1988
A; Title: The N terminus of laminin A chain is homologous to the B chains.
A; Reference number: S00624; MUID: 88225080; PMID: 3267223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;<sup>°</sup>
3-1389;1449-1459 <HA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: $08895
A, Molecule type: protein
A, Residues: 153-169 < MAN>
R, Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 222, 453-461, 1988
A, Title: Structure and distribution of N-linked oligosaccharide chains on various domain: A, Reference number: $02678; WUD: 88326259; PMID: 2458101
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Modecule type: protein
A, Residues: 630-642, 'D', 644;2690-2704 «FUJ»
R, Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
R, Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
B, Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaeumer, I.; Hartl, L.
A, Title: Stachem. 177, 35-45, 1988
A, Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-tes
A, Reference number: S01790; MUID: 89030693; PMID: 3181157
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A; Residues: 1911-1939;1977-2006;2013-2045, X', 2047-2054, X', 2056-2066, X', 2068-2105;2120
A; Residues: 1911-1939;1997-2006;2013-2045, X', 2593-2594;2600-2610;2616-2645;2648-2655;
93;2998-3005, A', 3007-3013, Y', 3035;3068-3083 <DE2>
A; Note: 2256-Val was also found
A; Note: 2256-Val was also found
Lab. Invest. 60, 772-782, 1989
A; Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A; Reference number: A34961; MUID:89280632; PMID:2733383
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A;Residues: 244-2416;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2.
-2942,'T'.294-2964;2962-2975;2980-2993;2998-3000,'I'.3002-3018,'V'.3020-3034;3068-3083
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin a
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C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
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                                                                                                                          C;Species: Mus musculus (house mouse)
C;Spaces: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A31771; A30449; S00624; A30450; S08895; S02678; S01790; A30451; S14670
C;Accession: A1771; A161man, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and A;Reference number: A31771; MUID:89034134; PMID:3182802
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A;Residues: 1-200'T',210-334 <HAR>
A;Cross-references: EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:g52858
A;Accession: A30450
                                                                                            Alternate names: laminin chain Al
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A,Molecule type: mRNA
A,Residues: 2538-3084 <DEU>
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R. Agopanguon, T.W.; Kokoza, V.A.; Cho, W.L.; Raikhel, A.S.

Proc. Natl. Acad. Sci. U.S.A. 93, 8934-8939, 1996

A. Title: Molecular characterization of the mosquito vitellogenin receptor reveals unexpe
A. Reference number: Z18874; MUID: 96392343; PMID: 8799131

A. Accession: T18308

A. Statue: pre-liminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
A. Residues: 1-1847 <SAP>
A. Gross-references: UNIPROT: 076952; EMBL: L77800; NID: 93386582; PID: 93386583; PIDN: AAC284
C. Function:
A. Description: involved in endocytosis
F. A5-79/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F. 84-120/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F. 132-167/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F. 956-987/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F. 132-167/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F. 101-249/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F. 1089-1124/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F. 1089-1124/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F. 1147-1212/Domain: LDL9
                                                                                                                                                                                                                                                                                                                                                      A59180
What inhibitory factor-1 - human
C;Species: Homo sapiens (man)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: A59180
R;Heite, J.C.; Kodplabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C.H.
Nature 399, 431-436, 1999
A;Title: A new secreted protein that binds to Wnt proteins and inhibits their activities
A;Reference number: A59180; WUID:99215557; PMID:10201374
A;Accession: A59180
A;Scatus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:Q9Y5W5; GB:AF122922; NID:94585369; PIDN:AAD25402.1; PID:9458
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C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18308
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.5; DB 2; Length 379;
Pred. No. 3.4;
2; Mismatches 16; Indels 1:
    Indels
    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
2; Mismatches
                                                                                                                                                  SPYEDEPC--RPCNCDPVGSLSSVCI
                                                                                            SPFEVPPCRSRDCRCVPIGLFVGFCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.2%;
33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 38.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 33.5
Matches 19, Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ADCNGAC-----
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12;
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R.Harris, B.
submitted to the EMBL Data Library, December 1996
A.Reference number: Z19165
A.Reference number: Z19165
A.Reference number: Z19165
A.Reference number: Z19165
A.Restus: preliminary; translated from GB/EMBL/DDBJ
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-1018 vMIL>
A.Residues: 1-1018 vMIL>
A.Residues: 1-1018 vMIL>
A.Residues: UNIPROT:P90769; EMBL:Z83220; PIDN:CAB05700.1; GSPDB:GN00019; CESP:C3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiHsia, R.; Bavoil, P.M.
Gene 176, 155-162, 1996
A;Title: Sequence analysis of the omp2 region of Chlamydia psittaci strain GPIC: Structur
A;Reference number: JC5203, MUID:97075924; PMID:8918247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 78/1; 149/1; 177/1; 245/1; 271/1; 311/2; 361/2; 387/3; 415/2; 444/3; 486/2; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij,
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                                                                                                                                                                                                                                                     hypothetical protein C34B7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer membrane protein 3 precursor - Chlamydophila psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 31-Mar-2000
C;Accession: JC5203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: S18994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the EMBL Data Library, February 1992
A;Description: The CDNA clonining and mRNA expression of rat protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <HSI>A;Residues: GB:U41759; NID:g1783376; PIDN:AAB41142.1; PID:g1783381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DC--NGACSPFEVPPCR--SRDCRCVPIGLFVGFCIHPTG 37
                                                     25 DCCFEDPCAPKPCNPCGNKKDKGCSPCGVYTPSCSKPCG 63
   2 DC--NGACSPFEVPPC-RSRDCRCVPIGLFVGFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 CHNYCHPGOTPPIPQRQPLVRCYDCESSDSDCFTGSC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57.5; DB 2; Dred. No. 29; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CNGACSPFEVPPCRSR-----DCRCVPIGLFVGFC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: omp3
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: clone C34B7 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: strain GPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:C34B7.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
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F;218-2893/Domain: laminin G repeat homology <LG2>
F;218-2893/Domain: laminin G repeat homology <LG2>
F;218-2893/Domain: laminin G repeat homology <LG3>
F;218-2893/Domain: laminin G repeat homology <LG4>
F;218-2893/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;45,79,310,347,310,365,2672,808,914,959,969,1052,1344,1414,1586,1603,1659,1686,1706,1718 e (Asn) (covalent) #status experimental F;70,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status experi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Chlamydophila psittaci, Chlamydia psittaci

C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004

C;Accession. A39439

R;Everett, K.D.E.; Hatch, T.P.

J; Bacteriol. 173, 3821-3830, 1991

A;Title: Sequence analysis and lipid modification of the cysteine-rich envelope proteins

A;Reference number: A39439; MUID:91267949; PMID:2050637
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                                                                                                                      F.34-401/Domain: v. Accousts
F.34-401/Domain: v. Accousts
F.404-458/Domain: laminin-type EGF-like homology <LEGOS
F.404-458/Domain: laminin-type EGF-like homology <LEGOS
F.404-458/Domain: laminin-type EGF-like homology &LEGOS
F.510-519/Domain: laminin-type EGF-like homology #status atypical <LEGOS
F.716-146/Domain: laminin-type EGF-like homology &LEGOS
F.749-95/Domain: laminin-type EGF-like homology <LEGOS
F.790-955/Domain: laminin-type EGF-like homology #status atypical <LEGOS
F.790-7-1116/Domain: laminin-type EGF-like homology #status atypical <LEGOS
F.790-7-1116/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1168/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOAA>
F.7106-1166/Domain: laminin-type EGF-like homology <mathematical account in the ADOA
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A39439
small cysteine-rich envelope protein envA precursor - Chlamydophila psittaci
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F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
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Pred. No. 46;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 87;
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4.2;
                          F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology
F;278-519/Domain: V <DOM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%; Score 57.5; Di
33.3%; Pred. No. 4.2;
tive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heptad repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;2134-3084/Domain: G < DOMG>
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Best Local Similarity
Matches 11; Conserv
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Matches 13; Conserv
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A; Residues: 1-87 < EVE>
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us-09-674-496d-8.rpr

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A Experimental source: calf liver

A Note: 49-11e was also found

C; Comment: The vertebrate metallothioneins contain two metal-binding domains. Clusters o

C; Comment: Cysteine clusters can also chelate univalent metal ions. As many as 18 differ

C; Superfamily: metallothionein

C; Superfamily: metallothionein

C; Keywords: accetylated amino end; chelation; metal binding; metal-thiolate cluster

F; 1-29/Domain: beta. < MH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;30-61/Domain: alpha <ALP>
F;1/Noditied site: acctylated amino end (Met) #status experimental
F;5/13.15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F;33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S00808; 146414; 746559
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel A;Reference number: S00808; MUID:88254812; PMID:3383853
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A; Molecule type: DNA
A; Residues: 1-61 <PET1>
A; Cross-references: UNIPROT: P04356; GB: X04626; NID: g4218467; PIDN: CAA28299.1; PID: g42184
                                                                                                                                                     C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
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Bur. J. Blochem. 160, 579-585, 1986
A;Title: Structure and regulation of the sheep metallothionein-Ia gene.
A;Reference number: 146414; MUID:87053978; PMID:3780723
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                                                                                                                                                                                                                           C;Accession: A03279
R;Winge, D.R.; Gray, W.R.; Zelazowski, A.; Garvey, J.S.
Arch. Biochem. Biophys. 245, 254-262, 1986
Arch. Biochem. Biophys. 245, 254-262, 1986
A;Title: Sequence and antigenicity of calf metallothionein II.
A;Reference number: A03279; MUID:86129456; PMID:3947100
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R;Peterson, M.G.; Lazdins, I.; Danks, D.M.; Mercer, J.F.
Bur. J. Biochem. 143, 507-511, 1984
A;Title: Cloning and sequencing of a sheep metallothionein A;Reference number: 146559; MUID:85003624; PMID:6434305
A;Accession: 146559
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A;Molecule type: DNA
A;Residues: 1-49,'S',51-61 <PET2>
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Pred. No. 8.4;
4; Mismatches
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A;Residues: 1-61 <WIN>
A;Cross-references: UNIPROT:P04356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.6%;
Matches 9; Conservative
                                                                                    netallothionein II - bovine
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A;Residues: 1-61 <PET3>
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A;Status: preliminary
A;Residues: preliminary
A;Residues: J-461 <0KA2>
A;Residues: 1-461 <0KA2>
A;Coss-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
A;Cross-references: EMBL:Xc4336; NID:g56962; PIDN:CAA45617.1; PID:g56963
C;Superfamily: ocagulation factor X; EGP homology; Gla domain homology; C;Reywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F;1-32/Domain: signal sequence #status predicted <SIG>
F;27-85/Domain: Gla domain homology <GLA>
F;33-42/Domain: propeptide #status predicted <PRO>
F;31-45/Domain: EGF homology <EG1>
F;91-130/Domain: EGF homology <EG1>
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A, Readiudes: 1-965 cAND>
A, Residues: 1-965 cAND>
A, Experimental source: strain S288C
A, Experimental source: strain S288C
R, Experimental source: strain S288C
S, Duesterhoeft, A.; Rloeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
Submitted to the Protein Sequence Database, April 1996
A, Reference number: S62944
A; Molecule type: mRNA
A; Residues: 1-461 < OKA>
A; Residues: 1-461 < OKA>
A; Residues: 1-461 < OKA>
A; Cross-references: UNPROT: P31394; EMBL: X64336; NID: 956962; PIDN: CAA45617.1; PID: 956963
R; Okafuji, T.; Maekawa, K.; Marumoto, Y.
Biochim: Biophys. Acta 1131, 329-332, 1992
A; Title: The CDNA cloning and mRNA expression of rat protein C.
A; Reference number: S24312; MUID: 92329550; PMID: 1627650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;139-174/Domain: EGF homology <EG2>
F;139-174/Domain: trypain: trypain homology <TRY>
F;213-485,50main: trypain homology <TRY>
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;213-130,135-135,161-114,182-320,239-255,373-387,388-426/Disnlfide bonds: #stat
F;215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;254,300,402/Active site: His, Asp, Ser #status predicted
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A;Cross-references: EMBL:Z71299; NID:g1301854; PID:e239870; PID:g1301855; MIPS:YNL023c
A;Experimental source: strain S288C
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S62935
Nypothetical protein YNL023c - yeast (Saccharomyces cerevisiae)
Nypothetical protein YNL023c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein N2812
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S62935; S62945
R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers, S.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62920
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Pred. No. 64;
2; Mismatches
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42.3%; Pred. No. 27;
Mismatches
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1 Similarity 30.4%;
14; Conservative
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A; Map position: 14L
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Best Local Similarity
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A;Cross-references: UNIPROT:018285; EMBL:Z82083; PIDN:CAB04972.1; GSPDB:GN00021; CESP:ZKJ
A;Experimental source: clone ZK1010
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[IgG Fc binding protein - mouse (fragment)
[IgG Fc binding protein - mouse mouse)
[Igg Fc becies was musculus (house mouse)
[Igg Fc becies 12-0ct-1999 #sequence_revision 22-0ct-1999
[Igg Fc becies 130257
[Igg Fc becips by 130257
[Igg Fc becips become 13025]
[Igg Fc become 13
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:P46CB.4
A;Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507
629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1
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A,Molecule type: mRNA
A,Residues: 1-1023 <TOM>
A,Cross-references: EMBL:AJ011416; NID:e1325179; PID:e1325180; PIDN:CAA09618.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ZK1010.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
24.3%; Score 54; DB 2; Length 2195;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 2; Mismatches 4; Indels
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A;Introns: 36/1; 71/1; 111/1; 175/2; 197/3; 237/1; 270/2; 308/3
                                                                                                                                                                                                            A,Molecule, type: DNA
A,Residues: 1-2195 <WIL>
A,Cross-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
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A;Description: The sequence of C. elegans cosmid F46C8. A;Reference number: 221497
A;Accession: T34264
A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, November 1996
A;Reference number: 220398
A;Accession: T27643
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 < WILL>
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128 NRKCSPYEAPPFRYTFCTRDTNRLAILGMYM 158
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A, Gene: CESP: ZK1010.6
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$500809
metallothionein Ib - sheep
metallothionein Ib - sheep
c;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 18-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
R;Petcrson, M.G.; Hannan, F.; Mercer, J.F.B.
Bur. J. Biochem. 174, 417-424, 1988
A;Titles: The sheep metallothionain gene family. Structure, sequence and evolutionary rel
A;Reference number: $00808; MUID:88254812; PMID:3383853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metallothionein Ic - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: 800810
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Bur. J. Biochem. 174, 417-424, 1988
A;Title: The sheep metallothionain gene family. Structure, sequence and evolutionary rel
A;Reference number: 800808; MUID:88254812; PMID:3383853
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-61 < PET>
A; Cross-references: UNIPROT: P09578; EMBL: X07974; NID: g1340; PIDN: CAA30786.1; PID: g1341
C, Genetics:
A; Introns: 10/1; 32/1
C; Superfamily: metallothionein
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T34264
T34264
Lypothetical protein F46CB.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34264
E;Wilcox, L.
S;Wilcox, L.
Submitted to the EMBL Data Library, November 1995
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                                                                                                                        DB 2; Length 61;
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Pred. No. 8.4;
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                                                                                                                   Query Match
24.3%; Score 54; DB 2
Best Local Similarity 34.6%; Pred. No. 8.4;
Matches 9; Conservative 4; Mismatches
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Best Local Similarity 34.6%
                     C; Superfamily: metallothionein
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les 9; Conservative
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A; Residues: 1-61 <PET>
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C;Accession: A44984
R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N.
Mol. Biochem. Parasitol. 37, 73-86, 1987
A;Title: Cuticle collagen genes of Haemonchus contortus and Caenorhabditis elegans are h A;Reference number: A44984; MUID:90136718; PMID:2615789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disobable cell-surface protein (cysteine-rich repeat motif) - Trypanosoma cruzi
N;Alternate names: hypothetical protein DGF-1
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A48450; S27852
R;Wincker, P.; Murto-Dovales, A.C; Goldenberg, S.
Mol. Blochem. Parasitol. 55, 217-220, 1992
Mol. Blochem. Parasitol. 55, 217-220, 1992
A;Title: Nucleotide sequence of a representative member of a Trypanosoma cruzi dispersed
A;Reference number: A48450; MUID:93063053; PMID:1435871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-3229 <WI2>
A;Cross-references: UNIPROT:Q26912; EMBL:M90534; NID:g162051; PID:g162052
A;Cross-reference extracted from NCBI backbone (NCBIP:118407)
C;Superfamily: Trypanosoma cruzi probable cell-surface protein (cysteine-rich repeat mot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A90701; A33725; C42175
R;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 15-Sep-2003
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
                                                                                                               Length 140;
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69.2%; Pred. No. 2.5e+02;
ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                 5 GACSPFE-----VPPCRSRDC-----RCVPIG 26
                                                                                                               Score 53; DB
Pred. No. 21;
6; Mismatches
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Pred. No. 38;
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39.1%;
                                                                                                               Query Match 23.9%;
Best Local Similarity 31.2%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Haemonchus contortus
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Best Local Similarity 39.17
Best Local Similarity 39.17
Conservative
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les 9; Conserv
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A; Residues: 1-295 <SHA>
A;Map position: 4
A;Introns: 26/1; 73/1
A;Note: T10114.60
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                                                                                                      hypothetical protein ZK783.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34513
R;Favello, A.; Vaudin, M.
submitted to the BMBL Data Library, August 1994
A;Description: The sequence of C. elegans cosmid ZK783.
A;Reference number: Z21536
A;Accession: T34513
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3507 <FAV>
A;Cross-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK
A;Experimental source: strain Bristol N2; clone ZK783
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104904
hypothetical protein T10114.60 - Arabidopsis thaliana
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjSpecies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CjAccession: T04904
R. Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A2389

Metallothionein 1 - bovine (tentative sequence)

C;Species: Bos primigenius taurus (cattle)
C;Species: Dos primigenius taurus (cattle)
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23889
R;Mungar, K.; Germann, U.A.; Beltramini, M.; Niedermann, D.; Baitella-Eberle, G.; Kagi, J. Blol. Chem. 260, 10032-10038, 1985
A;Title: (Ch.Zn)-metallothioneins from fetal bovine liver. Chemical and spectroscopic pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 3
A,Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2;
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A;Cross-references: UNIPROT:O49628; EMBL:AL021712
A;Experimental source: cultivar Columbia; BAC clone T10114
C;Genetics:
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Pred. No. 2.3e+02;
5; Mismatches 5;
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C;Superfamily: metallothionein
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Best Local Similarity 42.3%;
Matches 11; Conservative
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A;Molecule type: protein
A;Residues: 1-61 <MUN>
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les 9; Conserv
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                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-3566 -BRL>
A;Residues: 1-3566 -BRL>
A;Creal, Y: Bristow, J: Gitelman, S.E.; Miller, W.L.
B;Morel, Y: Bristow, J.; Gitelman, S.E.; Miller, W.L.
A;Crean Sci. U.S.A. 86, 6582-6586, 1989
A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c
A;Reference number: A33725; MUID:89367293; PMID:2475872
                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 2748-3199, V', 3201-3298, E', 3299-3314, G', 3316-3566 <MOR>
A;Residues: CB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070
A;Cross-references: GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070
R;Matsumoto, K.; Araj, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.
Genomics 12, 485-491, 1992
A;Title: Cluster of fibronectin type III repeats found in the human major histocompatibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 6p21.3-6p21.3
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: extracellular matrix; glycoprotein
J. Cell Biol. 122, 265-278, 1993
A/ILLE: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene A/Reference number: A40701; MUID:93300909; PMID:7686164
A/Accession: A40701
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F;748-828(Domain: Elbronectin type III repeat homology <3F1>
F:829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>
F;873-953/Domain: fibronectin type III repeat homology <3F3>
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A;Residues: 1849-1936 <MAT>
A;Residues: asource: clone 3.9kF3-1
A;Note: sequence extracted from NCBI backbone (NCBIP:95694)
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A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB
A;Cross-references: GDB:568487; OMIM:600261
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RESULT 25

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C;Accession: T09070
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Scł aubmitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: 216543
A;Reference number: Z16543
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: TXX
A,Map position: 17
A,Map position: 17
A,Map position: 17
A,Introns: 124/1; 735/1; 773/3; 826/1; 914/1; 1037/1; 1135/1; 1232/1; 1329/1; 1440/1; 15.
A,Introns: 124/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3646/1; 3694/1; 3737/3; 3: 0.19/1; 3115/1; 3208/1; 3302/1; 3405/1; 3517/1; 3558/1; 3606/1; 3694/1; 3737/3; 3: C; Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type: C; Superfamily: EGF homology <EGF>
F; 422-448/Domain: EGF homology <EGF>
F; 826-906/Domain: fibronectin type III repeat homology <3FR>
F; 826-906/Domain: fibrinogen beta/gamma homology <FEGS>
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A;Cross-references: UNIPROT:035452; EMBL:AF030001; NID:92564945; PID:92564958
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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47.6%; Pred. No. 3e+02;
tive 2; Mismatches
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Best Local Similarity 47.6
Matches 10; Conservative
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US-09-907-8B1-4
US-09-907-8B3-4
Sequence 167170, Sequence 210838, Sequence 256220, Sequence 12, Appl Sequence 572087, Sequence 653, Appl Sequence 20, Appl Sequence 20, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 10, Appl
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Compugen Ltd
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shou Yinha
APPLICANT: Abu Yinha
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICANION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 101
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Publication No. US20040055038A1

GENERAL INPORMATION:

APPLICANT: KNAUF, VIC C.

APPLICANT: KNAUF, VIC C.

APPLICANT: KRIDL, JEAN C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION TITLE OF INVENTION: MUMBER: US/09/782,130

CURRENT APPLICATION NUMBER: US 09/232,861

PRIOR APPLICATION NUMBER: US 09/232,861

PRIOR APPLICATION NUMBER: US 08/484,941

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-06-05-21

PRIOR FILING DATE: 1990-05-21

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                                                                                                      Query Match 65.3%; Score 145; DB 15; Length 80; Best Local Similarity 64.9%; Pred. No. 2.6e-09; Matches 24; Conservative 4; Mismatches 9; Indels
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                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32413C.1.pep
US-10-424-599-210838
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US-10-424-599-269230
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        OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040031072A1
GENERAL INFORMATION:
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ORGANISM: Glycine max
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(101)
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US-10-424-599-269230
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBUCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 167170
LENGTH: 127
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Sequence 210838, Application US/10424599

Sequence 210838, Application US/10424599

Publication No. US20440031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: Acou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILNG DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 210838
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US-10-424-599-167170
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US-10-028-072-308
US-10-10-808-308
US-10-121-049-308
US-10-123-904-308
US-10-175-746-308
US-10-176-918-308
US-10-176-918-308
US-10-002-73-22
US-10-066-273-22
US-10-066-494-22
US-10-137-86-308
US-10-140-474-308
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ORGANISM: Glycine max
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Best Local Similarity
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ORGANISM: Glycine max
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NAME/KEY: unsure
LOCATION: (1)..(80)
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GENERAL INFORMATION AND OSCUPIOLISTANDAL GENERAL INFORMATION TO USE OSCUPIOLISTANDAL GENERAL INFORMATION TO USE OSCUPIOLISTANDAL STANDAL SAPLICANT: BOUKharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Brad Standal S
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Sequence 5, Application US/09938275

Sequence 5, Application US/09938275

GENERAL INFORMATION:

APPLICANT: Gerardo Castillo

APPLICANT: Alan Snow

TITLE OF INVENTION: Therapeutic and Diagnostic Applications

TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments

FILE REFERENCE: PROTEO.P03

CURRENT APPLICATION NUMBER: US/09/938,275

CURRENT FILING DATE: 2001-08-16

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 3075
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46.2%; Pred. No. 1.5e+02;
tive 2; Mismatches 10; Indels
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Pred. No. 4;
5; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Swissprot P25391
US-09-938-275-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 187490, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.6%;
Matches 14; Conservative
          NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.2
Matches 12, Conservative
                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-764-868-653
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -10-437-963-187490
                                                                                                              TYPE: PRT
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(53223)
TILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO S: 285684
SEQ ID NO S: 272087
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PRIOR FILING DATE: 1988-11-02
PRIOR APPLICATION NUMBER: US 06/692,605
PRIOR PILING DATE: 1985-01-17
PRIOR PELING DATE: 1980-09-14
PRIOR APPLICATION NUMBER: US 07/582,241
PRIOR APPLICATION NUMBER: US 07/188,361
PRIOR PELING DATE: 1988-04-29
PRIOR PELING DATE: 1988-04-15
PRIOR APPLICATION NUMBER: US 07/168,190
PRIOR PILING DATE: 1988-03-15
Remaining Prior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 35.
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Pred. No. 1.5;
2; Mismatches 10; Indels 7
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT APPLICATION NUMBER: US/09/764,868

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism: Protease OTHER INFORMATION: inhibitor Palb peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 34.2%; Score 76; DB 11; Length 18; Best Local Similarity 64.7%; Pred. No. 0.057; Matches 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_87713C.1.pep
US-10-424-599-272087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 SOCSGGCSOTPFPKPCLFFFKCSKKCLCVPPGFF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 272087, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 653, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
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Best Local Similarity 45...
Best Local Similarity 65...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Unknown Organism
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ORGANISM: Glycine max
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APPLICANT: SLOUGH, JANIE 0.7;
APPLICANT: Taupier, Raymond J.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE.
FILE REFERENCE: 12402-538B
CURRENT APPLICATION NUMBER: US/10/357,820
FRIOR PEDICATION NUMBER: US/10/357,820
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/730617
PRIOR APPLICATION NUMBER: 09/730617
PRIOR PELLING DATE: 2002-02-12
PRIOR PELLING DATE: 2002-06-01
PRIOR PELLING DATE: 2002-06-06
PRIOR PELLING DATE: 2002-06-06
PRIOR PELLING DATE: 2002-06-07
PRIOR PELLING DATE: 2002-08-07
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 8
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Pred. No. 26;
2; Mismatches 16; Indels 19;
                                                       Sequence 8, Application US/10357820 Publication No. US20040029140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10357820
Publication No. US20040029140A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Li, Li;
Padigaru, Muralidhara;
                                                                                                                                                                                                                                                                                                                                                                                      Shimkets, Richard A.;
Stone, David J.;
                                                                                                                                                                           Casman, Stacie J.;
Gorman, Linda;
Ji, Weizhen;
Kekuda, Ramesh;
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Casman, Stacie J.;
Gorman, Linda;
Ji, Weizhen;
Kekuda, Ramesh;
Li, Li;
                                                                                                                                                                                                                                                                                                                Patturajan, Meera,
Pena, Carol E.A.;
Shenoy, Suresh G.;
                                                                                                                           APPLICANT: Anderson, David W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.2%;
33.9%;
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Best Local Similarity 33.9
Matches 19; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-538B
                                                                                                                           ij
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SOFTWARE: CuraSeqList version 0.1
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                                                                             Length 77;
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                                                                                                                        Indels
; OTHER INFORMATION: Clone ID: PAT_MRT4530_84188C.1.pep
US-10-437-963-187490
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6
                                                                          DB 16;
                                                                   Query Match 28.2%; Score 62.5; D
Best Local Similarity 46.2%; Pred. No. 7;
Matches 12; Conservative 0; Mismatches
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Pred. No. 25;
2; Mismatches
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Padigaru, Muralidhara,
Padigaru, Merai
Pena, Carol E.A.;
Shenoy, Suresh G.;
Shimkets, Richard A.;
Stone, David J.;
                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10357820 Publication No. US20040029140A1
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, David W.;
APPLICANT: Burgess, Catherine E.;
APPLICANT: Casman, Steace J.;
APPLICANT: Gorman, Linda;
APPLICANT: Ji, Weizhen;
APPLICANT: Kekuda, Ramesh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%;
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Best Local Similarity 33.5
Matches 19; Conservative
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US-10-357-820-20
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LENGTH: 337
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APPLICANT: Ji, Weizhen;
APPLICANT: Kekuda, Ramesh;
APPLICANT: Edvida, Ramesh;
APPLICANT: Padigaru, Muralidhara;
APPLICANT: Padigaru, Muralidhara;
APPLICANT: Patturajan, Meera;
APPLICANT: Pena, Carol E.A.;
APPLICANT: Shankete, Richard A.;
APPLICANT: Shankete, Richard A.;
APPLICANT: Stone, David J.;
APPLICANT: Stone, David J.;
APPLICANT: Taupier, Raymond J.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD PILE REPERENCE: 21402-538B
CURRENT APPLICATION NUMBER: US/10/357,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω,
                                             PRIOR PILING DATE: 2002-02-10;
PRIOR PLILALICATION NUMBER: 10/13858
PRIOR PILING DATE: 2002-05-01
PRIOR PILING DATE: 2002-05-01
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-08-07
PRIOR PILING DATE: 2002-08-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-08-07
PRIOR PILING DATE: 2002-08-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.2%; Score 62.5; DB 15; Length 365; Best Local Similarity 33.9%; Pred. No. 27; Matches 19; Conservative 2; Mismatches 16; Indels 19
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PRIOR APPLICATION NUMBER: 60/387002
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-02-08
                      APPLICATION NUMBER: 10/074978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10357820 Publication No. US20040029140A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-357-820-6
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APPLICANT: Shinkets, Richard A.;
APPLICANT: Shinkets, Richard A.;
APPLICANT: Shinkets, Richard A.;
APPLICANT: Shinkets, Richard A.;
APPLICANT: Scone David J.;
APPLICANT: A Taugler, Raymond J.
FILE REFERENCE: 21402-538
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/673460
PRIOR PILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/730617
PRIOR APPLICATION NUMBER: 00/387002
PRIOR APPLICATION NUMBER: 60/387002
PRIOR APPLICATION NUMBER: 60/387002
PRIOR APPLICATION NUMBER: 60/387002
PRIOR APPLICATION NUMBER: 60/38709
PRIOR PILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/38209
PRIOR PILING DATE: 2002-04-25
PRIOR PLING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/38265
PRIOR PLING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/38265
PRIOR PLING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/381666
PRIOR APPLICATION NUMBER: 60/381666
PRIOR PLING DATE: 2002-06-07
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APPLICANT: Patturajan, Meera;
APPLICANT: Patturajan, Meera;
APPLICANT: Patturajan, Meera;
APPLICANT: Sheno, Suresh G.;
APPLICANT: Shonoy, Suresh G.;
APPLICANT: Stone, David J.;
APPLICANT: Taupier, Raymond J.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-538B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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Pred. No. 27;
2; Mismatches 16; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ADCNGAC------GFCIHPTG 37
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CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/679460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, David W.;
APPLICANT: Burgess, Catherine E.;
APPLICANT: Caeman, Stacke J.;
APPLICANT: Gorman, Linda;
APPLICANT: Ji, Weizhen;
APPLICANT: Kekuda, Ramesh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.2%;
Best Local Similarity 33.9%;
Matches 19; Conservative
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APPLICANT:
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APPLICANT: Shenoy, Suresh G.;
APPLICANT: Shimkets, Richard A.;
APPLICANT: Stone, David J.;
APPLICANT: Taupier, Raymond J.
TILE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE
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CURRENT APPLICATION: THERAPEDITIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAM
FILE REFERENCE: 21402-538B

CURRENT APPLICATION NUMBER: US/10/357,820

FRIOR PILING DATE: 2003-02-03

FRIOR PILING DATE: 2000-12-06

FRIOR FILING DATE: 2000-12-05

FRIOR PILING DATE: 2000-12-05

FRIOR PLILING DATE: 2000-06-01

FRIOR PLILING DATE: 2002-02-12

FRIOR PLILING DATE: 2002-05-01

FRIOR PLILING DATE: 2002-06-01

FRIOR FILING DATE: 2002-06-07

FRIOR APPLICATION NUMBER: 60/381666

FRIOR FILING DATE: 2002-06-17

FRIOR APPLICATION NUMBER: 60/381666

FRIOR FILING DATE: 2002-06-17

FRIOR APPLICATION NUMBER: 60/381666

FRIOR FILING DATE: 2002-06-17

FRIOR APPLICATION NUMBER: 60/381666

FRIOR PROPERMARE: CLASSEGLISH VERSION 0.1

FROM APPLICATION NUMBER: 60/381666

FRIOR APPLICATION NUMBER: 60/381666

FRIOR FILING DATE: 2002-06-17

FRIOR APPLICATION NUMBER: 60/381666

FRIOR APPLICATION NUMBER: 60/3816
                                                                                                                                                                                                                                                                                                                                                                                                                                               176 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 231
                                                                                                                                                                                                                                                                                Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 231
                                                                                                                                                                                                                                                                                                                                                                    ----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
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                                                                                                                                                                                                 Length 375;
                                                                                                                                                                                             28.2%; Score 62.5; DB 15; 33.9%; Pred. No. 28; ive 2; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/10357820
Publication No. US20040029140A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, David W.; APPLICANT: Burgess, Catherine E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li, Li;
Padigaru, Muralidhara;
Patturajan, Meera;
Pena, Carol E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess, Catherine B
Casman, Stacie J.;
Gorman, Linda;
Ji, Weizhen;
Kekuda, Ramesh;
                                                                                                                                                                                    Query Match
Best Local Similarity 33.99
Matches 19; Conservative
                     ; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    1 ADCNGAC----
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                                                                                                     US-10-357-820-12
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APPLICANT: Shimkets, Richard A.;
APPLICANT: Shimkets, Richard J.;
APPLICANT: Taugier, Raymond J.
TITLES OF INVENTION: THERABEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL FILE REFERENCE: 21402-538
CURRENT APPLICATION NUMBER: 09/679460
FRIOR APPLICATION NUMBER: 09/679460
FRIOR FILING DATE: 2000-10-04
FRIOR PRILING DATE: 2000-10-04
FRIOR PAPLICATION NUMBER: 10/074978
FRIOR PILING DATE: 2002-02-01
FRIOR APPLICATION NUMBER: 60/387002
FRIOR PILING DATE: 2002-06-07
FRIOR PILING DATE: 2002-06-07
FRIOR PILING DATE: 2002-06-07
FRIOR PILING DATE: 2002-04-05
FRIOR PIL
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PRIOR FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/393265
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2002-08-07
PRIOR PRIOR APPLICATION NUMBER: 60/381666
PRIOR FILING DATE: 2002-05-17
PREmaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 95
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 95 SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 62.5; DB 15; Length 373; 33.9%; Pred. No. 28; Live 2; Mismatches 16; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/10357820; Publication No. US20040029140A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Anderson, David W.;
PAPLICANT: Burgess, Catherine B.;
APPLICANT: Casman, Stacie J.;
APPLICANT: Gorman, Linda;
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Pena, Carol E.A.;
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Kekuda, Ramesh;
Li, Li;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.2
Best Local Similarity 33.9
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-10-357-820-12
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APPLICANT: WOOG, WILLIAM, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14

CURRENT PAPLICATION NUMBER: US/09/909,088B

CURRENT FILING DATE: 2001-07-18

PRIOR PILING DATE: 1090-07-07

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR PAPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21697
                                                                                                                                                                                                                                                                  180 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 235
                                                                                                          Score 62.5; DB 9; Length 379;
Pred. No. 28;
2; Mismatches 16; Indels 19; Gaps
                                                                                                                                                                                                                           ---SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
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APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, P. Mickey
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                28.2%;
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                          Query Match
Best Local Similarity 33.9
Matches 19; Conservative
                                                                                                                                                                                                                           1 ADCNGAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fong, Sherman
Gao, Wei-Qiang
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, A.
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APPLICANT:
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Deniel
APPLICANT: Williams, Deniel
APPLICANT: Wood, William, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14 ANDER: US/09/903,20
CURRENT APPLICATION NUMBER: US/09/903,20
CURRENT PILING DATE: 2000-01-04
PRIOR APPLICATION NUMBER: US 60/145,696
PRIOR APLICATION NUMBER: US 60/145,696
PRIOR APLICATION NUMBER: US 60/146,222
PRIOR APLICATION NUMBER: US 60/146,222
PRIOR APLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-01-15
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1990-11-30
PRIOR PIL
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Grimaldi, Christopher J.
                                                                                ; Sequence 4, Application US/09909320; Patent No. US20020132240Al; GENERAL INFORMATION:
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                             RESULT 16
US-09-909-320-4
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APPLICANT:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
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US-09-902-853-4
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APPLICANT:
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-27
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 379
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FILING DATE: 1999-07-28
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: US 60/143,048
APLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-07
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/145,698
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-909-088B-4
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                      PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PLICATION NUMBER: PCT/US99/28313
PRIOR PLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR PE
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 33.9
Matches 19; Conservative
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US-09-905-291A-4
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Transmembrane Polypeptides and Nucleic
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                                                                                                           APPLICANT: 'Undean', Darkey
APPLICANT: 'Undean', Descreted and Transmembrane P TITLE OF INVENTION: Secreted and Transmembrane P TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT PAPLICATION NUMBER: 09/665,350
PRIOR PAPLICATION NUMBER: 09/665,350
PRIOR PELING DATE: 2000-09-18
PRIOR FILING DATE: 12000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
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Pred. No. 28;
2; Mismatches
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PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR FLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PRIOR DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-13-30
PRIOR PLING DATE: 1999-13-30
PRIOR PLING DATE: 3000-01-05
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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Publication No. US20020198366A1
GENERAL INFORMATION:
                             oy, Margaret Ann
tewart, Timothy A.
umas, Daniel
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33.9%;
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Demoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 33.9
Matches 19; Conservative
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ORGANISM: Homo Sapien
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Pred. No. 28;
2; Mismatches 16; Indels
                                             PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-01
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PRIOR DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
FILING DATE: 2000-09-18
APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
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Publication No. US20020197671A1
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1 Similarity 33.9%;
19; Conservative :
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Baton, Duc
APPLICANT: Baton, Du
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Gao, Wei-Qiang
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ORGANISM: Homo. Sapien
US-09-902-853-4
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Best Local Similarity
Matches 19; Conserv
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LPLICANT: Williams, P. Mickey
LPPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Acids encoding the same CURRENT APPLICATION NUMBER: US/09/904,011
CURRENT FILING DATE: 2001-07-11
PRIOR PEDICATION NUMBER: US/09/904,011
PRIOR PEDICATION NUMBER: 109/665,350
PRIOR PELING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-22
PRIOR PELING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-00
PRIOR PELING DATE: 1999-13-00
PRIOR PELING DATE: 199
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Mather, Jennie P.
          Filvaroff, Ellen
                                               ong, Sherman
ao, Wei-Qiang
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; ORGANISM: Homo Sapien
US-09-904-011-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2001-01-20
PRIOR PLING DATE: 2000-02-22
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
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33.9%; Pred. No. 28;
iive 2; Mismatches 16; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/09904011; Publication No. US2003003530A1; GENERAL INPORMATION:
; APPLICANT: Genentech, Inc.; APPLICANT: Botstein, David; APPLICANT: Besterin, David; APPLICANT: Eaten, Dan L.; APPLICANT: Eaten, Dan L.; APPLICANT: Ferrara, Napoleone
                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Garber, Hangpeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 33.9
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-09-907-841-4
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### APPLICATION NUMBER: US 091414400.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/908,093

CURRENT PILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US/66,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15
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Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
SEQ ID NOS: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                           Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                Gurney, Austin L.
Hillan, Kenneth, J
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                                                                                                   Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Best Local Similarity 33.9
Matches 19; Conservative
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ORGANISM: Homo Sapien
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US-09-906-742-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCWNGGLCVTPGFCICPPG 235
  180 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 235
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Pred. No. 28;
2; Mismatches 16; Indels 19;
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CURRENT PEPLICATION NUMBER: US/09/903,640
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 4
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Publication No. US20030017498A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betteelin, David
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                     Sequence 4, Application US/09903640 Publication No. US20030017463A1 GENERAL INFORMATION:
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Wood, William, I.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betselin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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ORGANISM: Homo Sapien
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Best Local S
Matches 19
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Indels 19; Gaps

US-09-906-742-4

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APPLICAWY: Williams, wannes, wannes, admiss, wannes, applicawy: Williams, walliam, i TTTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TTTLE OF INVENTION: Acide Encoding the Same CIRRENT APPLICATION: Acide Encoding the Same PTLE REFERENCE: 104664. William, i CIRRENT APPLICATION NUMBER: US/09/906,742

CURRENT FILING DATE: 2001-07-16 65.350

PRIOR APPLICATION NUMBER: 006/143,048

PRIOR PLINKO DATE: 1999-07-28

PRIOR PLINKO DATE: 1999-07-18

PRIOR PLINKO DATE: 1999-07-18

PRIOR PLINKO DATE: 1999-01-15

PRIOR PLINKO DATE: 1999-01-15

PRIOR PLINKO DATE: 1999-11-29

PRIOR PRILOR PLINKO DATE: 1999-11-29

PRIOR PLINKO DATE: 1999-11-29

PRIOR PLINKO DATE: 1999-11-29

PRIOR PLINKO DATE: 1999-11-30

PRIOR PRIOR PLINKO DATE: 1999-11-30

PRIOR PLINKO DATE: 1999-11-30

PRIOR PLINKO DATE: 1999-11-30

PRIOR PRILOR PLINKO NUMBER: PCT/US99/3091

PRIOR PLINKO DATE: 1999-11-30

PRIOR PRILOR PRIDE: 1999-11-30

PRIOR PRILOR PRICE: 1999-11-30

PRIOR PRINCE: 1999-11-30

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Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
                                                                                                                                                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Publication No. US20030023054A1
GENERAL INFORMATION:
                                                            APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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TYPE: PRT ORGANISM: Homo Sapien

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  Query Match 28.2%; Score 62.5; DB 10; Length 379; Best Local Similarity 33.9%; Pred. No. 28; Matches 19; Conservative 2; Mismatches 16; Indels 19;
Length 379;
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Sequence 19, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 1280, Appl Sequence 1280, Appl Sequence 1280, Appl Sequence 14, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 1786, Appl Sequence 17, Appl Sequence 18, Appl Sequence 56, Appl Sequence 57, Appl Sequence 57, Appl Sequence 18, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 20, Appl Sequence 19, Appl Sequence 10, Appl 
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Sequence
Sequence
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US-09-252-991A-26163
US-09-252-991A-21561
US-09-252-991A-30732
US-09-006-353A-6
US-09-573-986-6
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US-09-949-016-9775
US-09-949-016-9775
US-09-198-428-557
US-09-438-185A-560
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US-09-252-991A-30404
US-09-252-991A-30404
US-09-32-991A-3511
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US-09-252-991A-17866
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US-09-252-991A-30774
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US-07-668-648-4
US-08-429-998-4
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US-08-848-631-2
US-08-848-631-5
US-09-902-540-10793
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US-09-068-624-1
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US-09-422-869-18
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US-09-824-647-17
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Sequence 15, Appl
Sequence 5, Appli
Sequence 5, Appli
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                                                                                                                       March 28, 2005, 08:51:20 ; Search time 30 Seconds (without alignments) 92.067 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/SB_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/ROMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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222
1 ADCNGACSPPEVPPCRSRDCRCVPIGLFVGFCIHPTG
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S-09-252-991A-17820
S-09-252-991A-26035
S-09-538-092-650
S-09-270-767-34799
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-09-575-081B-12
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Maximum Match 100%
Listing first 100 summaries
                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                                                            protein
                                                                                                                                                                                                                                      Sequence:
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Result No.

Nucleic Acids Encoding Merosin, Merosin Fragments and Uses Thereof

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                                                                                                                    Sequence 15, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%; Score 63; DB 2; Length 243; 46.2%; Pred. No. 5.6; tive 2; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
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FILING DATE:
CLASSIFICATION: 435

RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 21-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 30-JAN-1990
FRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO:
TELEPHONE: (619) 535-9901
TELEFRAX: (619) 535-9901
TELERPAX: (619) 535-9001
TELERPAX: (619) 535-9001
TELERPAX: (619) 535-9849
INFORMATION FOR SEQ ID NO:
TENAMETION FOR SEQ ID NO:
TENAMETION FOR SEQ ID NO:
TELERPAX: (619) 535-9849
ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 243 amino acids
amino acid
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Best Local Similarity 46.2
Matches 12; Conservative
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STATE: California
                                                                                                 JS-08-460-309-15
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Sequence 15, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo

US-08-125-077-15

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Gaps
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APPLICANT: Engvall, Eva
APPLICANT: Engvall, Eva
APPLICANT: Engvall, Eva
APPLICANT: Engvall, Eva
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.4%; Score 63; DB 2; Length 243; Best Local Similarity 46.2%; Pred. No. 5.6; Matches 12; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                             STATE: CALIFOLIDA
COUNTE: CALIFOLIDA
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIPTCATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
FILING DATE: 21-SEP-1994
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 31-UL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
RESISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
RESIDENCE/DOCKET NUMBER: 31,815
RESIDENCE/DO
TITLE OF INVENTION: Nucleic Acids Encoding Merosi TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23 CORRESCONDENCE ADDRESS: ADDRESSEE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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Gaps

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
SEQUENCE CHARACTERISTICS:
LENGTH: 3075 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 SPYEDEPC--RPCNCDPVGSLSSVCI 410
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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Grimaldi, Christopher J.
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Patent No. 6635468
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.45
Best Local Similarity 46.25
Matches 12; Conservative
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard, A.
                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    US-08-125-077-5
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APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Pragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

28.4%; Score 63; DB 2; Length 3075;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 12; Conservative 2; Mismatches 10; Indels
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ZIP: 92122

ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077

**ILING DATE: 22-SEP-1993
***TLING DATE: 24-SEP-1993
                                                 CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 1,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPRAM: (619) 535-9001
TELEPRAM: (619) 535-9001
TELEPRAM: 3075 amino acids
WANTE: amino acids
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CLASSIFICATION: 435
RIGN APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
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  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
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US-08-125-077-5
; Sequence 5, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
STATE: California
COUNTRY: USA
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APPLICANT:
APPLICANT:
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               PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
APPLICATION NUMBER: PCT/US99/21547
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Conservative
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ORGANISM: Homo sapiens
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Matches 19; Conserve
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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| PRIOR FILING DATE: 1999-07-07
| PRIOR PAPLICATION WURBER: US 60/145,222
| PRIOR PILING DATE: 1999-07-26
| PRIOR PILING DATE: 1999-09-13
| PRIOR PILING DATE: 1999-09-13
| PRIOR PILING DATE: 1999-09-13
| PRIOR PAPLICATION NUMBER: PCT/US99/21090
| PRIOR APPLICATION NUMBER: PCT/US99/21090
| PRIOR PAPLICATION NUMBER: PCT/US99/21090
| PRIOR PAPLICATION NUMBER: PCT/US99/21014
| PRIOR PAPLICATION NUMBER: PCT/US99/30011
| PRIOR PAPLICATION NUMBER: PCT/US99/30
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APPLICANT: Batch and APPLICANT: Batch and APPLICANT: Bernard B

Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P.

Pan, James Paoni, Nicholas F

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same
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28.2%; Score 62.5; DB 4; Length 379;
Best Local Similarity 33.9%; Pred. No. 9.6;
Matches 19; Conservative 2; Mismatches 16; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ACIDS BICCOLLING LIE SABING CURRENT APPLICATION NUMBER: US/09/906,700 CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/09/906,700 PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-13-03

PRIOR PILING DATE: 1999-13-03

PRIOR PILING
                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.
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Kljavin, Ivar J.
Mather, Jennie P.
                                                                  Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                       Paoni, Nicholas F.
                                        Gerber, Hanspeter
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ORGANISM: Homo sapiens
US-09-906-700-4
                                                                                                       Goddard, A.
                                                                                                                                                                                                                                                                                                                                                  Pan, James
                                                                                                                                           APPLICANT
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                                                                     ## APPLICANT: Tunnas, Daniel
## APPLICANT: Willians, P. Mickey
## APPLICANT: Willians, P. Mickey
## APPLICANT: Wood, Willian, I.
## TITLE OF INVENTION: Acids Encoding the Same
## TITLE OF INVENTION: Acids Encoding the Same
## CURRENT FILMS OF THE ## SOUTH OF 10
## CURRENT FILMS OF THE ## SOUTH OF 10
## RIOR APPLICATION NUMBER: US/09/902,775A
## RIOR APPLICATION NUMBER: US/09/00/0414
## RIOR APPLICATION NUMBER: US/09/00/0414
## RIOR APPLICATION NUMBER: US/09/01/09/04
## RIOR APPLICATION NUMBER: US/09/01/09/04
## RIOR APPLICATION NUMBER: US/09/01/03/09/04
## RIOR PILING DATE: 1999-07-28
## RIOR PILING DATE: 1999-07-38
## RIOR PILING DATE: 1999-10-03
## RIOR APPLICATION NUMBER: PCT/US99/2865
## RIOR PILING DATE: 1999-10-03
## RIOR PILING DATE: 1999-12-03
## RIOR PILING DATE: 1999-13-03
## RIOR PILING DATE: 1999-13-03
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
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; ORGANISM: Homo sapiens
US-09-902-775A-4
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APPLICANT:
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APPLICANT:
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US-09-903-603A-4
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-26
PRIOR PRILING DATE: 1999-07-28
PRIOR PRILING DATE: 1999-07-13
PRIOR PRILING DATE: 1999-09-13
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-09-15
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-03
PRIOR PRIPOR DATE: 1999-12-03
PRIOR PRIPOR DATE: 1999-12-03
PRIOR PRIPOR DATE: 1999-12-03
PRIOR PRIPOR
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Grimaldi, Christopher J.
                   4, Application US/09903603A
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Sao, Wei-Qiang
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ORGANISM: Homo sapiens
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                                                   Patent No. 6767995
GENERAL INFORMATION:
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                                                                             1 ADCNGAC------GPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                                      16; Indels 19;
  DB 4; Length 379;
Score 62.5; DE
Pred. No. 9.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Grimaldi, Christopher J. APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth, J. APPLICANT: Hillan, Kenneth, J. APPLICANT: Hillan, Ivar J. APPLICANT: Mather, Jennie P. APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and TransmITLE OF INVENTION: Acids Encoding the
                                                                                                                                                                                                                 Sequence 4, Application US/09904920A Patent No. 6806352
                                                                                                                                                                                                                                                                                                                                                                          Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
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Query Match
Best Local Similarity 33.9
Matches 19; Conservative
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APPLICANT: Vulliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-06-229
PRIOR APPLICATION NUMBER: US 60/143,048
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                                                                         | PRIOR FILING DATE: 1999-10-05
| PRIOR PELICATION NUMBER: PCT/US99/28214
| PRIOR PELICATION NUMBER: PCT/US99/28313
| PRIOR PELICATION NUMBER: PCT/US99/28313
| PRIOR PILING DATE: 1999-11-30
| PRIOR PILING DATE: 1999-12-02
| PRIOR PELICATION NUMBER: PCT/US99/28565
| PRIOR PELICATION NUMBER: PCT/US99/30095
| PRIOR PELICATION NUMBER: PCT/US99/30095
| PRIOR PELICATION NUMBER: PCT/US99/30911
| PRIOR PELICATION NUMBER: PCT/US99/30911
| PRIOR PELICATION NUMBER: PCT/US99/30911
| PRIOR PELING DATE: 1999-12-20
| PRIOR PELING DATE: 2000-01-05
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E.
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Mather, Jennie P.
                                                                 LING DATE: 1999-10-05
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Botstein, David
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Best Local Similarity 33.9
Matches 19; Conservative
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Eaton, Dan L.
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US-09-905-381A-4
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-013
PRIOR PILING DATE: 1999-09-013
PRIOR PILING DATE: 1999-09-013
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Pred. No. 9.6;
2; Mismatches 16; Indels 19
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
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Patent No. 6818449
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Ashkenazi, Avi
Botstein, David
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                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-4
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                 LENGTH: 379
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: 10466-114
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
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Pred. No. 9.6;
2; Mismatches 16; Indels 1
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 4
                                                                                                                                                                                                                                                                       PRIOR FILLING DATE: 2001-07-16
PRIOR FILLING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-09-09
PRIOR PILING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-11-29
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                                                            Williams, P. Mickey Wood, William, I.
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33.9%;
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Matches 19; Conservative
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ORGANISM: Homo sapiens
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             PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/20944
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-11-20
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
PRIOR PELING DATE: 1999-12-07
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Grimaldi, Christopher J.
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Patent No. 6828146
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Hillan, Kenneth, J.
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Goddard, A.
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FILING DATE: 1999-07-07
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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ORGANISM: Homo sapiens
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Best Local Similarity
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ER APPLICATION NUMBER: 60/048, 892
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048, 915
ER APPLICATION NUMBER: 60/049, 019
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048, 970
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048, 970
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048, 972
ER PILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048, 972
ER PILING DATE: 1997-06-06
                                                                                                                                                                                                                                       R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,876
R FILING DATE: 1997-06-06
R PILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,895
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R APPLICATION NUMBER: 60/048,917

R APPLICATION NUMBER: 60/048,949

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,974

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,974
                                                                              R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,880
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,896
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R FILING DATE: 1997-06-06

A APPLICATION NUMBER: 60/048,964

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

A APPLICATION NUMBER: 60/048,882

R FILING DATE: 1997-06-06

PILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,898
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APPLICATION NUMBER: 60/048,962
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/092,921
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APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/049,374
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APPLICATION NUMBER: 60/048,897
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APPLICATION NUMBER: 60/048,894
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FILING DATE: 1997-06-06
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                            TLING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,881
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APPLICATION NUMBER: 60/048,971
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EARLIER REARLIER BEARLIER BEAR
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NAME/KEY: SITE
LOCATION: (296)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08460309
Patent No. 5837466
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
ITILE OF INVENTION: Nucleic Acids Encoding Merosin
TITLE OF INVENTION: Nucleic Acids Encoding Merosin
TITLE OF INVENTION: Pragments and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.2%; Score 62.5; DB 4; Length 380; 33.9%; Pred. No. 9.7; tive 2; Mismatches 16; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURREALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 32-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: US 07/472,319
FILING DATE: US 07/472,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (380)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-441
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
BARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
BARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 441
LENGTH: 380
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.9
Matches 19, Conservative
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ADCNGAC----
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LOCATION: (264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SITE
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96 PAAFVPAASTDĆMQIAITDFTAFCVFPT 123
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                              118 SPYDDHPC--RPCNCDPVGSLSSVCI 141
      8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-14078
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LENGTH: 722
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; Sequence 16, Application US/08125077
; Patent No. 5872231
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Pragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                             26.6%; Score 59; DB 2; Length 243; 42.3%; Pred. No. 16; tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59, DB 2; Length 243;
Pred. No. 16;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PULGATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUU-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-849
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 42.3%;
Matches 11; Conservative
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Best Local Similarity 42.39
Matches 11, Conservative
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STATE: California
COUNTRY: USA
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US-08-125-077-16
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Sequence 14078, Application US/09489019A

Sequence 14078, Application US/09489019A

Sequence 14078, Application US/09489019A

Sequence 14078, Application US/09489019A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 14078

LENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RDCRCVPIGLFVG 30
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Sequence 12, Application US/09575081B
Fatent No. 6692934
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
FILE REPERBENCE: DB23
CURRENT FILING DATE: 2000-05-19
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 90/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 90/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR APPLICATION NUMBER: 60/135,081
FRIOR PRICE PROFILED NUMBER: 90/135,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 722;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.7%; Score 57; DB 4
Best Local Similarity 27.9%; Pred. No. 74;
Matches 17; Conservative. 1; Mismatches
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US-09-270-767-50016

Sequence 50016, Application US/09270767

Sequence 50016, Application US/09270767

Sequence 50016, Application US/09270767

SEGUENCE No. 6703491

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 50016

LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                      Score 54.5; DB 4; Length 965;
Pred. No. 1.9e+02;
2; Mismatches 17; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 CORKCHPGKCPPCLESDSNDLVCPCGNTVVPAPVRCGTKLPTCNHP 518
                                                                                                                                                                                                                                                                                                                                                                                                       3 CNGACSPFEVPPCRSRD----CRC-----VPIGLFVGFCIHP 35
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  ; SEQ 1D NO 650
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YNL023C
US-09-518-092-650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.3%; Score 54; DB 4;
Best Local Similarity 39.4%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 AGAAAACHPAQIPGGCIGRRCHCLGIGR-PGLC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AGAAAACHPAQIPGGCIGRRCHCLGIGR-PGLC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ADCNGACSPFEVP-PCRSRDCRCVPIGLFVGFC 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Drosophila melanogaster
US-09-270-767-34799
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US-09-270-767-50016
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.4%;
Matches 14; Conservative
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Best Local Similarity :
"**rches 13; Conservat
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LENGTH: 178
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Patent No. 6551795

GENERAL INCOMPATION:

RAPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MURBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

RIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26035
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132 FOR CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR PILING DATE: 1999-02-18 PRIOR RPLICATION NUMBER: US 60/074,788 PRIOR RPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1999-02-18 PRIOR FILING DATE: 1999-07-27 NUMBER: US 62/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 17820 LENGTH: 195
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APPLICANT: Giot Loic
APPLICANT: Giot Loic
APPLICANT: Giot Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/120,352
PRIOR APPLICATION NUMBER: 60/120,352
PRIOR APPLICATION NUMBER: 60/120,352
PRIOR SPEING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 ASCSTATAPVACCSATPVPPCRASPSANCTPI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ADCNGA-----CSPFEVPPCR-SRDCRCVPI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55.5; D
Pred. No. 33;
1; Mismatches
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Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.8%;
Matches 14; Conservative
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Pred. No. 50;
5; Mismatches 7; Indels
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24.3%; Score 54; DB 3; Length 199;
Best Local Similarity 28.6%; Pred. No. 50;
Matches 16; Conservative 5; Mismatches 7; Indels
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            US-09-23-2191-19
US-09-23-2191-19
Patent No. 6284487
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Bavid J.
APPLICANT: Lodalsh, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WH197-21p3ME
CURRENT APPLICATION NUMBER: US/09/232,191
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
FARLIER PILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20

EARLIER FILING DATE: 1998-07-20

SARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 37

LENGTH: 199

LENGTH: 199
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APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHISP-21paMs
CURRENT PELLICATION NUMBER: 05/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER PELLING DATE: 1998-01-15
EARLIER PELLING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-10-10
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FREEESQ for Windows Version 3.0
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Best Local Similarity 28.6
Matches 16; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
-09-232-191-19
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This sequence represents the Cys-rich peptide sequence of legume plant derived insecticidal peptide PAlb corresponding to that of an entomotoxic pea protein. The invention relates to a novel insecticidal peptide PT (AAYS5990) isolated from pea plants which has homology to the PAID peptide and to the leginsuline from soybeans (AAYS5991). The insecticidal peptides preferably have the amino acid sequence:

XICySX2CySX3CySX4CySX5CySX6CySX7 where XI = 2-10 amino acids; XS = 2-5 amino acids; XS = 7-15 amino acids; XA = 3-10 amino acids; XS = 2-4 amino acids; XS = 7-15 amino acids; and X7 = 2-10 amino acids; B = 2-4 amino acids; A = 3-10 amino acids; A = 3-10
                                                                                                            Consensus, plant, legume, insecticide, entomotoxic, pea, cereal, grain, pest, Sitophilus oryzae, Ephestia kuehniellea, Acyrthosiphon pisum; genetically modified organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of polypeptide as insecticide, especially for controlling cereal grain pests.
                                                                                                                                                                                                                                                                                                                                                                                                             Grenier A, Gueguen J, Ferrasson E,
                                                                         Insecticidal peptide PAlb from pea plants.
                                                                                                                                                                                                                                                                                                                                                        (NASC-) INST NAT SCI APPLIQUEES LY
(INRG ) INST NAT RECH AGRONOMIQUE.
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                                          15-MAR-2000 (first entry)
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es 23; Conserv
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                                                                                                                                                                                 Pisum sativum
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Best Local Si
Matches 23;
         AAY55991,
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   Ada80464 Human
Ada75706 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of polypeptide as insecticide, especially for controlling cereal grain pests.
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100.0%; Pred. No. 2.2e-18;
iive 0; Mismatches 0;
                                                                       ALIGNMENTS
 ADA80464
ADA75706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NASC-) INST NAT SCI APPLIQUEES LYON.
(INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                       AAYSS992 standard; peptide; 37 AA.
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   9 9
                                                                                                                                                                                                                             (first entry)
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 379
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 28.2
28.2
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62.5
62.5
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Matches
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Mbailao M;

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                                                                                                                                                                                                                                                                         Consensus; plant; legume; insecticide; entomotoxic; pea; cereal; grain; pest; Sitophilus oryzae; Ephestia kuehniellea; Acyrthosiphon pisum; genetically modified organism.
                                 Gaps
                                 ;
0
    Length 37;
                               Indels
                                                                         ASCNGVCSPFEMPPCGTSACRCIPVGLVVGYCRNPSG 37
69.8%; Score 155; DB 3; L. 62.2%; Pred. No. 1.1e-10; Live 7; Mismatches 7;
                                                          1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37
                                                                                                                                                                                                                                              Insecticidal peptide PT from pea plants.
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                                                                                                                                                           AAY55990 standard; peptide; 37
                               Conservative
                                                                                                                                                                                                                                                                                                                                  Pisum sativum
                                                                                                                                                                                                                   15-MAR-2000
                                                                                                                                                                                      AAY55990;
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Gaps

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Indels

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1 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37 ADCNGACSPFEVPPCRSRDCRCVPIGLFVGFCIHPTG 37

ð 유 AAY55991 standard; peptide; 37 AA

RESULT 2 AAYS5991

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85US-00692605.
86US-00891529.
87US-00054369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                     Knauf VC, Kridl JC;
                                                                                                        (CALJ ) CALGENE LLC
                                                                                                                                                                    WPI; 2001-564354/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                                                                                                                   transcription.
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31-JUL-1986;
26-MAY-1987;
                              09-JUL-1990;
10-AUG-1993;
07-JUN-1995;
07-MAR-1997;
02-NOV-1988
21-MAY-1990
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 THE REAL PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                       Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11; 2A11; PA1B.
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                                                                                                                                                                                                                                                Use of polypeptide as insecticide, especially for controlling cereal
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                                                                                                                                                                                    Mbailao M;
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                                                                                                                                                                                    Gueguen J, Ferrasson E,
                                                                                                                                     (NASC-) INST NAT SCI APPLIQUESS LYON.
(INRG ) INST NAT RECH AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                             Example 2; Fig 7; 38pp; French
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87US-00054369.
87US-00078538.
88US-00147781.
88US-00168190.
                                                                           99WO-FR001085
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22; Conservative
                                                                                                                                                                                   Delobel B, Grenier A,
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26-MAY-1987;
28-JUL-1987;
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15-MAR-1988;
29-APR-1988;
                                                                           07-MAY-1999;
                                                                                                       11-MAY-1998;
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                WO9958695-A1
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                                             18-NOV-1999
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The invention provides a method for obtaining a plant which produces at least one seed having a modified phenotype. The method involves transforming a host plant cell with a DNA construct which consists of operably linked components in the direction of transcription, a promoter region from a Brassica plant gene, a DNA sequence of interest other than the native coding sequence, and a transcription termination region. The method is useful for obtaining plants having modified phenotype or for altering the phenotype of a plant seed or tissue. The DNA constructs are used in manipulating plant cells to provide for regulated transcription, such as light inducible transcription, in a plant tissue or plant part of interest at particular stages of plant growth or in response to external control. These constructs are also used for modulation of expression of endogenous products as well as production of exogenous products in the seed. Sequences AABB8936-13 represent fragments of storage proteins used in comparison studies with the storage protein 2A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obtaining a plant that produces a seed with a modified phenotype or altering a seed phenotype, comprises transforming a plant cell with a D construct consisting of operably linked components in the direction of
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88US-00267685.
90US-00526123.
90US-00550804.
93US-00105852.
95US-00484941.
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14-SEP-2000;
                                                                                                                                                                                                                                                     02-AUG-2001
        The invention relates to a DNA construct comprising, as operably linked components in the direction of transcription, a promoter region of components in the direction of transcription, a promoter region of containing an age of an acyl carrier protein (ACP) gene, a DNA sequence of interest other than the native components are functional in a plant cell and where the DNA construct is flanked by T-DNA. Also included are a plant cell having an altered phenotype as a result of expression of a DNA construct, a plant comprising a plant by a plant by a plant to impart a desired characteristic to seed as comprising a plant to impart a desired characteristic to seed as plant, obtaining a plant to impart a desired characteristic to seed as construct from other plant tissue, altering the phenotype of plant seed tissue and selectively expressing a heterologous DNA sequence of there are the plant tissue and selectively expressing a heterologous DNA sequence of the regulating genetic modification of plant to construct is useful in modifying or altering the genotype or phenotype of a plant to impart a desired characteristic. The construct is also useful construct is useful in modifying or altering the genotype or phenotype of a plant to impart a desired characteristic. The construct is also useful construct is useful in modifying or altering the genotype or phenotype or pendeced have increased capability of protein storage, improved nutrient construct in the hartient from charten means and construct in the plants of construct and plants and dehydration resistance and construct and construct are constructed response to light and dehydration resistance and construct and plants or means and construct and plants or means and construct and con
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                                                                                                                                                                                                                                                                                                                          New DNA construct comprising a promoter region, a DNA sequence of interest and a transcription termination region, useful for producing transgenic plants.
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87US-00078538.
88US-00147781.
88US-00168190.
88US-00188361.
88US-00267685.
90US-00526123.
                                                                                                         90US-00582241.
91US-00742834.
93US-00105852.
95US-00484941.
97US-00812665.
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                                                                                                                                                                                                                                                               Knauf VC, Kridl JC;
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                                                                                                                                                                                                                  (KNAU/) KNAUF V C.
(KRID/) KRIDL J C.
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                                                             02-NOV-1988
                                                                              21-MAY-1990
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chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS;
Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
              antinfilammatory, anti-HIV; antibacterial; antinfilammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition, organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; daucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                        acquired immune deficiency syndrome.
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2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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2000US-0217496P.
2000US-0218290P.
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2000US-0220964P.
2000US-0224518P.
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2000US-0225213P.
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2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
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2000US-0232400P.
2000US-0232401P.
2000US-0233064P.
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2000US-0233065P.
2000US-023423P.
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2000US-023498P-
2000US-0235834P-
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2000US-0235836P-
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2000US-0246611P-
2000US-0249207P-
2000US-0249208P-
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2000US-0249212P.
2000US-0249213P.
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2000US-0241826P.
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2000US-0246478P.
2000US-0246523P.
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2000US-0246527P.
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14-SEP-2000; 214-SEP-2000; 214-SEP-2000; 214-SEP-2000; 214-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 27-SEP-2000; 2
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17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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The invention relates to novel isolated polypeptides (I), and definition relates to novel isolated polypeptides (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune confirmations organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepaticis (), bleeding disorders, hemoglobin abnormalities and cother blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (C.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (c.g. Gaucher's disease), achoemic injury (e.g. stroke), renal disorders (e.g. capithelial cell proliferation, endocrine disorders (e.g. arrhythmia), cardiovascular disorders (e.g. arrhythmia), capithelial cell proliferation, endocrine disorders (e.g. Addisease), reproductive system disorders (cirrhosis), as stimulators of disease), reproductive system disorders (cirrhosis), as stimulators of cirrhosis, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AMU17059.
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                                                                                                                                                                                                                                                                                                                                               Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 653; 880pp; English
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                                06-DEC-2000; 2000US-0251479F.

08-DEC-2000; 2000US-025186F.

08-DEC-2000; 2000US-0251869F.

08-DEC-2000; 2000US-0251869F.

08-DEC-2000; 2000US-0251999F.

11-DEC-2000; 2000US-0251990F.
                                                                                                                                                                         05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                N-PSDB; AAS27005
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ADB93796
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Homo sapiens.

14-NOV-2002

14-AUG-2000;

14-AUG-2000; 14-AUG-2000; 30-AUG-2000;

22-AUG-2000;

SEP-2000;

-SEP-2000;

SEP-2000;

21-SEP-2000;

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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the presence or amount of expression of the polypeptide is also useful for identifying a binding partner and determining whether the binding partner of the polypeptide. The polypeptide is useful for identifying a binding partner and determining whether the binding partner of effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliocating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid encoding a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USPTO at segdata.uspto.gov/sequence.html?DocID=20020168711.
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23-AUG-2000; 2000US-00649167.
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ABG12917
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2000US-0220963P.
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2000US-0224518P.
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2000US-0235834P.
2000US-0236327P.
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2000US-0234274P.
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N-PSDB; ADB93173.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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biodiversity.
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Matches
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                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypoperide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at

Company of the printed specification, but was obtained in company of the company of the
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diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                             Claim 20; SEQ ID NO 43276; 103pp; English.
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23-AUG-2000; 2000US-00649167.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colympopide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders (involving aberrant protein expression or biological activity. The colympopide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations creponable for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
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food supplement; medical imaging; diagnostic; genetic disorder
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Claim 20; SEQ ID NO 40113; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1216 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001.
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WPI; 1998-240534/21.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are also assess biodiversity and account of the constant of the mapping, identification of mutations and constant of the constant 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.4%; Score 63; DB 4; Length 2901; 46.2%; Pred. No. 2.1e+02;
Claim 20; SEQ ID NO 40122; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2901 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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5 10; Indels 2; Mismatches 387 SPYEDEPC--RPCNCDPVGSLSSVCI 410 8 SPFEVPPCRSRDCRCVPIGLFVGFCI 33 12; Conservative Matches g à

ä

Gaps

AAW50892 standard; protein; 3075 AA (first entry) Human laminin A chain. 07-DEC-1998 AAW50892; RESULT 11 AAWS0892 ID AAWS 

Laminin, human; beta-amyloid; amyloidosis; Alzheimer's disease; Down's syndrome; hereditary cerebral haemorrhage; inflammation; malignancy; Familial Mediterranean Fever; multiple myeloma; type II dlabetes; prion disease; Creutzfeldt-Jacob disease; CJD; Gertsmann-Straussler syndrome; kuru; scrapie; haemodialysis; carpal tunnel syndrome; senile cardiac amyloid polyneuropathy; Familial Amyloidotic Polyneuropathy; thyroid carcinoma; diagnosis; therapy.

Homo sapiens

2690. .2700 /noce= "beta-amyloid protein binding region (Claim 12)" /note= "fourth globular domain repeat (Claim 12)" Location/Qualifiers Region Domain g k

WO9815179-A1

97WO-US018145. 08-OCT-1997; 16-APR-1998.

96US-0027981P. 08-OCT-1996;

(UNIW ) UNIV WASHINGTON.

Castillo G,

Snow AD;

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This is the amino acts sequence of the numan laminin derived protein object of the invention is to use laminin, laminin-derived protein cobject of the invention, deposition, accumulation and/or persistence in amyloid formation, deposition, accumulation and/or persistence in Alzheimer's disease and other amyloidoses. The laminin products (see AMWEG0889-98) may include mouse or human laminin A chain, laminin BI corresponded to the laminin A chain and (merosin), laminin Glorain, laminin BI comprises of the laminin A chain and the beta-amyloid binding domain of the laminin A chain, A claimed method for treating an amyloid disease comprises administering a polypeptide having a conformational similarity to a fragment of a laminin protein. A method for diagnosing an amyloid disease involves determining levels of laminin in a sample. Production of disease involves determining levels of laminin in a sample. Production of laminin or its fourth globular repeat in vivo provides a method for in vivo inhibition of beta-amyloid amyloidosis. The products and methods can be used for the dispnosis, monitoring and treatment of amyloidoses such as Alzheimer's disease, bown's syndrome and hereditary crebral haemorrhage with amyloidosis of the Dutch type (where the amyloidoses such as Alzheimer's disease, bown's syndrome and hereditary crebral haemorrhage with multiple myelome and other B-cell Mediterranean Fever (AA amyloid or inflammation-associated with type II consormalities (AL amyloid), the amyloidosis associated with type II consormalities (AL amyloid), the amyloidosis associated with prion disease, Gertetmann-Straussler Syndrome, kuru and animal scrapie (PrP amyloidosis associated with engaled and sease including Creutzfeldt-Jacob disease, Gertetmann-Straussler Syndrome, kuru and animal scrapie (PrP amyloidosis associated with engaled and panilal Amyloidosis associated with engaled a
                                                                                                                                                                                                                                                                       is the amino acid sequence of the human laminin A chain. The primary
                                                                                  Use of laminin and fragments - for developing products for use in the diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or
                                                                                                                                                                                                           Claim 15; Page 80-85; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 procalcitonin)
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Sequence 3075 AA;

Gaps .. 7 Length 3075; 10; Indels 28.4%; Score 63; DB 2; I 46.2%; Pred. No. 2.2e+02; ive 2; Mismatches 10; Query Match
Best Local Similarity 46.2
Matches 12; Conservative

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ADF44673 standard; protein; 337 12-FEB-2004 (first entry) ADF44673; RESULT 12 

Human NOV1j protein SEQ ID NO:20.

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human; antidiabetic; anorectic; cardiant; hypotensive;

antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelminthic; nootropic; neuroprotective; antihelminthic; nootropic; neuroprotective; antihelminthic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; vulnerary; antianglogenic; gene therapy; metabolic disorder; diabetes; obesity; antianglogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; haematopoietic disorder; inflammatory skin disorder; asthma; dyslipidaemia. щ ;

Gaps

19;

16; Indels

Mismatches

2

Conservative

19;

Matches

ð

1 ADCNGAC------GPEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37

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Claim 1; SEQ ID NO 20; 234pp; English.
                                                                                            01-MAY-2002; 2002US-00138588.
17-MAY-2002; 2002US-0381666P.
07-JUN-2002; 2002US-0387002P.
                                                                     19-FEB-2002; 2002US-035792BP.
21-FEB-2002; 2002US-035860BP.
27-FEB-2002; 2002US-035860B
25-APR-2002; 2002US-0375579P.
                                                                                                              02-JUL-2002; 2002US-0393265P.
07-AUG-2002; 2002US-0401825P.
                                        03-FEB-2003; 2003WO-US003403
                                                                                                                                            Burgess CE,
                                                                                                                                                  Padigaru M, Pa
J, Taupier RJ;
                                                                                                                                                                                                       asthma, or infections.
                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                  WPI; 2003-748127/70.
N-PSDB; ADF44672.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 337 AA;
                 WO2003066881-A2
      Homo sapiens
                                                          12-FEB-2002;
12-FEB-2002;
                                                                                                                                            Anderson DW,
                             14-AUG-2003
                                                                                                                                                   Li L, Pad:
Stone DJ,
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atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS; acquired immune deficiency syndrome; asthma; Crohn's disease; multiple sclerosis; anorexis; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; dyallipidaemia; wasting disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
diagnosis; NOVX-associated disorder; cardiomyopathy;
                                                                                                             ADO50858 standard; protein; 337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson DW, Burgess CE, Casman :
Li L, Padigaru M, Patturajan M,
Stone DJ, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-0359860P.
2002US-0375579P.
2002US-00138588.
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2002US-00074978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0381666P
                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; vaccine; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-2003; 2003US-00357820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002; 2002US-0393265P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00730617
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATTURAJAN M.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BURGESS C E.
CASMAN S J.
GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANDERSON D W.
                                                                                                                                                                                                                          Human NOV1j protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-179665/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STONE D J.
TAUPIER R J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PADIGARU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADO50857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004029140-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-2002;
21-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2002;
                                                                                                                                                                                        15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2002
                                                                                                                                                 ADO50858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHIM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAUP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PADI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PENA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JIWM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PATT/
                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n is a niteger between 1 and 34); (b) a mature form of (a); or (c) a conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic, anotropic, neuroprosective, antiparkinsonian, anticonvulsant, orteopathic, antiparkinsonian, anticonvulsant, orteopathic, antidiapemic, vulnerary and antiangiogenic activities, and antiasthmatic, antilipaemic, vulnerary and antiangiogenic activities, and antibodies that immunospecifically bind (I), can be used in the manufacture of a medicament for treating a syndrome associated with a human disease such metabolic disorders, disabetes, obseity, infectious diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), cardiovascular diseases (hypertension, atherosclerosis), enurodegenerative disorders, asthma, and various dyslipidaemias. (I) and interest entry asthmatory skin disorders, asthma, and various dyslipidaemias. (I) and small and about a the sequence for the identification of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in gene ration of antibodies that bind immunospecifically to (I) for use in therapeutic or diagnostic methods (I) can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                        Kekuda R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                      ss CE, Casman SJ, Gorman L, Ji W, F
Patturajan M, Pena CEA, Shenoy SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.5; I
Pred. No. 35;
                                                                                                                           2002US-00074978.
2002US-0356424P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes, atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and in chromosome mapping, tissue typing or pharmacogenomics.
   Kekuda R;
Shimkets RA;
JI W,
noy SG,
   Casman SJ, Gorman L, Ji
ijan M, Pena CEA, Shenoy
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Anderson DW

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'n
                                               The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiowypathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, infections, haemophilia, graft-versus-host disease, AIDS (acquired immune deficiency syndrome), asthma, Crohn's disease, multiple sclerosis, anorexia, cancer-associated cachexia, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, haematopoietic disorders, dyslipidaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; antidiabetic; anorectic; cardiant; hypotensive; antidiateriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelminthic; nootropic; neuroprotective; antiperkinsonian; anticonvulsant; osteopathic; antialipaemic; antilipaemic; antinflammatory; dermatological; antiasthmatic; antilipaemic; vulnerary; antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; ancreate, cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; ostecarthritis; hemitopoletic disorder; inflammatory skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 207
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         ADCNGAC------SPEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 337;
                                                                                                                                                                                                                                                                                                                                                  Score 62.5; DB 8; Length 33° Pred. No. 35; 2; Mismatches 16; Indels
                   Claim 1; SEQ ID NO 20; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADF44661 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human NOV1d protein SEQ ID NO:8.
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12-FEB-2002; 2002US-0356424P.
19-FEB-2002; 2002US-0357828P.
27-FEB-2002; 2002US-0359600P.
27-FEB-2002; 2002US-0359860P.
25-APR-2002; 2002US-0359860P.
                                                                                                                                                                                                                                                                                                                                                28.2%;
33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0355099P
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2002US-0401825P.
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                                                                                                                                                                                                                                                                                                                             Query Match
Bust Local Similarity 33.55,
Best Local 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoarthritis, haemat
asthma; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003066881-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where not is an integer between 1 and 34); (b) a mature form of (a); or (c) a conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:2(n.). (I) and (II) have antidiabetic, ancretic, cardiant, hypotensive, antiarteriosclerotic, ancretic, ancettic, antidiaperic, antidiaperic, antidiaperic, antidiaperic, antidiaperic, antidiaperic, antidiaperic, antidiamentory, dermatological, antidiathmatic, antidiaperic, and antidiaperic acid molecules (II) and antibodies that immunospecifically bind (I), can be used in gene therapy. The polypeptides (I), nucleic acid molecules (II) and antibodies that immunospecifically bind (I), can be used in the manufacture of a medicament for treating a syndrome associated with a chuman disease. They are useful for treating a syndrome associated with a chuman disease. They are useful for treating protozoal), anorexia, cancer, cardiovascular diseases (hypertension, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), cardiovascular diseases (setecarthritis), haematopoietic disorders, ephlepsy, immune disorders, asthma, and various dyslipidaemias. (I) and conting the manufacture of a transporter for the identification of small and a target for the identification of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in gene ration of antibodies that bind immunospecifically to (I) for use in therapeutic or diagnostic methods. (I) can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is used in the exemplification of the present invention.
    Kekuda R;
Shimkets RA;
                                                                                                                                                                New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS; acquired immune deficiency syndrome; asthma; Crohn's disease; multiple sclerosis; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; dyslipidaemia; wasting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy;
Casman SJ, Gorman L, Ji W,
ijan M, Pena CEA, Shenoy SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.5; I
Pred. No. 36;
                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 8; 234pp; English.
Burgess CE, Casman S
ru M, Patturajan M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.9,
....nes 19, Conservative
                           Padigaru M, Pa
J, Taupier RJ;
                                                                                                                                                                                                                                        asthma, or infections.
                                                                                              WPI: 2003-748127/70
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                                                                                                                    N-PSDB; ADF44660
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                             Li L, Padi
Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO50846;
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    8$XCCCCCCCCCCCCCCCCCCCCCX
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The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, infections, haemophilia, graft-versue-host disease, AIDS (acquired immune deficiency syndrome), asthma, Crohn's disease, multiple sclerosis, ancera, cancer-associated cachexia, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, haematopoietic disorders dyslipidaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridisation probes, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes, atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human NOVX protein.
 chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; gene therapy; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n DW, Burgess CE, Casman SJ, Gorman L, Ji W, Kekuda R;
Padigaru M, Patturajan M, Pena CEA, Shenoy SG, Shimkets RA;
J, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 8; 119pp; English
                                                                                                                                                                              05-DEC-2000; 2000US-00730507.

12-FEB-2002; 2002US-00730517.

13-FEB-2002; 2002US-0057928P.

21-FEB-2002; 2002US-0357928P.

21-FEB-2002; 2002US-0359860P.

25-APR-2002; 2002US-0359860P.

25-APR-2002; 2002US-0359860P.

17-MAY-2002; 2002US-0318588.

07-JUN-2002; 2002US-0381666P.

07-JUN-2002; 2002US-0381666P.
                                                                                                                                                                   2000US-00679460
                                                                                                                                    16-JUL-2003; 2003US-00357820
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LI L.
PADIGARU M.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENA C E A.
SHENOY S G.
SHIMKETS R A.
STONE D J.
TAUPIER R J.
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CASMAN S J.
GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-179665/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADO50845
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                                                                        US2004029140-A1
                                            Homo sapiens
                                                                                                                                                                   04-OCT-2000;
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Stone DJ,
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(PADI/)
(PATT/)
                                                                                                                                                                                                                                                                                                                                                                                                (CASM/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PENA/)
(SHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                              (JIMM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (KEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STON/)
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The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where n is an integer between 1 and 34); (b) a mature form of (a), or (c) a sequence that is at least 95% identical to (P), or having one or more conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, antihelminthic, nootropic, neuroprotective, antiparkinsonian, anticonvulsant,
                                                                                                                                                                                                                                            human; antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelannthic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antilipaemic; anticonvulsant; osteopathic; antilipaemic; anticonvulsant; osteopathic; antilipaemic; vulnerary; antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; betteostivitis; hematopoletic disorder; inflammatory skin disorder;
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Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
|:| | | AECPGGCRNGGFCNERRICGCPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casman SJ, Gorman L, Ji W,
ijan M, Pena CEA, Shenoy SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DW, Burgess CE, Casman :
Li L, Padigaru M, Patturajan M,
                                                                                                        ADF44659 standard, protein; 365
                                                                                                                                                                                                              Human NOV1c protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2002US-0355099P.
2002US-036424P.
; 2002US-035928P.
; 2002US-0359860P.
; 2002US-0359860P.
; 2002US-0375579P.
; 2002US-031566P.
; 2002US-039365P.
; 2002US-039365P.
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                                                                                                                                                                             12-FEB-2004 (first entry)
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J, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; dyslipidaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-748127/70.
N-PSDB; ADF44658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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12-FEB-2002;
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                                                                                                                                         ADF44659;
                                                                                       ADF44659
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1 ADCNGAC-----

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16; Indels 19;

Score 62.5; DB 8; Length 343; Pred. No. 36; 2; Mismatches 16; Indels 15

Query Match 28.2%; Best Local Similarity 33.9%; Matches 19; Conservative ;

----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37

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can be used in gene therapy. The polypeptides (I), mucleic activities, and antiasthmatic, antilipaemic, vulnerary and antiangiogenic activities, and can be used in gene therapy. The polypeptides (I), mucleic acid molecules (II) and antibodies that immunospecifically bind (I), can be used in the manufacture of a medicament for treating a syndrome associated with a confidence of the metabolic disorders, diabetes, obseity, infectious diseases (Viral, bacterial, fungal, helminthic, and protocoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), anorexia, cancer, cardiovascular diseases (Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders, Alzheimer's disease, Parkinson's disease, epilepsy, immune disorders, asthma, and various dyshipidaemias. (I) and continguation of unition of small (II) may also be used as targets for the identification of small (II) and differentiation, cell proliferation, hematopoiesis, wound healing and immunospecifically to (I) for use in therapeutic or diagnostic methods. (I) can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present continued the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; antidiabetic; anorectic; cardiant; hypotensive; antidiateriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelminthic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiparkinsonian; anticonvulsant; antiasthmatic; antilipaemic; vulnerary; antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; ancexia; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; haematopoletic disorder; inflammatory skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 62.5; DB 7; Length 36 33.9%; Pred. No. 38; ive 2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF44657 standard; protein; 365 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-0381666P.
2002US-0387002P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 365 AA;
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01-MAY-2002;
17-MAY-2002;
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02-JUL-2002;
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The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where not as an integer between 1 and 34); (b) a mature form of (a); or (c) a sequence that is at least 95% identical to (P), or having one or more conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic, ancretic, cardiant, hypotensive, antiarteriosclerotic, anorectic, or virucide, antibacterial, fungicide, protozoacide, antihalmithic, or virucide, antibacterial, fungicide, protozoacide, antihalmithic, costeopathic, antiarthritic, antihalminflammatory, dermatological, antisathmatic, antiharthritic, antihalminflammatory and antibacture of a medicament for treating a syndrome associated with a channal decrease. They are useful for treating a syndrome associated with a human disease such metabolic disorders, diabetes, obesity, infectious disease, controlegenerative disorders, halphalminflam, anticoscolerosis, cardiovascular diseases (Nypertension, atherosclerosis), anorexia, cancer, cardiovascular diseases (Nypertension, and various dyslipidaemias. (I) and differentiation, cell proliferation, thematopolesis, wound healing and angiogenesis, in gene targets for the identification of small differentiation, cell proliferation, heamatopolesis, wound healing and angiogenesis, in gene therapy, in gene ration of antibodies that bind inthe exemplification probes, in chromosome mapping, cell manusopecifically.
                                                                                           Kekuda R;
Shimkets RA;
                                                                                                                                                                                                                                          New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7; Length 365;
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                                                                                         Casman SJ, Gorman L, Ji W,
Jan M, Pena CEA, Shenoy SG,
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Local Similarity 33.9%; Pred. No. 38;
les 19; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4; 234pp; English.
                                                                                    Anderson DW, Burgess CE, Casman (
Li L, Padigaru M, Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO50844 standard; protein; 365 AA
  07-AUG-2002; 2002US-0401825P.
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                                                                                                           Padigaru M, Pa
J, Taupier RJ;
                                                                                                                                                                                                                                                                                                                   asthma, or infections.
                                          (CURA-) CURAGEN CORP
                                                                                                                                                                             2003-748127/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV1c protein.
                                                                                                                                                                                                N-PSDB; ADF44656.
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                                                                                                                              Stone DJ,
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Matches
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3;

Pred. No.

33.9%;

Local Similarity

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The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiomyopathy, at the respective of scleroderma, obseity, cancer diabetes, infections, haemophilia, graft-versus-host disease, AIDS (acquired immune deficiency syndrome), asthma, Crohn's disease, multiple sclerosis, anorexia, cancer-associated cachexia, neurodegenerative disorders anorexia, cancer-associated cachexia, haematopoietic disorders, dyslipidaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes, atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and in chromosome mapping, tissue typing or pharmacogenomics.
              multiple sclerosis; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; dyslipidaemia; wasting disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; gene therapy; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kekuda R;
Shimkets F
 acquired immune deficiency syndrome; asthma; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w,
SG,
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ou M, Patturajan M, Pena CEA, Shenoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1, SEQ ID NO 6; 119pp; English
                                                                                                                                                                                                                                        05-DEC-2000; 200005-0073510.

08-FEB-2002; 2002US-0073617.

12-FEB-2002; 2002US-0074978.

19-FEB-2002; 2002US-0357928P.

21-FEB-2002; 2002US-03598608P.

25-FEB-2002; 2002US-0359860P.

25-APR-2002; 2002US-0375579P.

01-MAY-2002; 2002US-0375579P.

07-JUN-2002; 2002US-0381666P.

07-JUN-2002; 2002US-0381666P.
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PENA.C E A.
SHENOY S G.
SHIMKETS R A.
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J, Taupier RJ;
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CASMAN S J.
GORMAN L.
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TAUPIER R J.
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N-PSDB; ADO50843.
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PADIGARU M.
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                                                                                                                                    JS2004029140-A1
                                                                                                          sapiens
                                                                                                                                                                    12-FEB-2004
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(CASM/)
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(PADI/)
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(TAUP/)
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                                                                                                                                                                                            atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS; acquired immune deficiency syndrome; asthma; Crohn's disease; multiple sclerosis; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; dyslipidaemia; wasting disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kekuda R;
Shimkets RA;
                                          Gaps
                             ----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
        19;
                                                                                                                                                                                   diagnosis; NOVX-associated disorder; cardiomyopathy;
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SG,
        Indels
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jan M, Pena CEA, Shenoy
        16;
        Mismatches
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                                                                                                    ADO50842 standard; protein; 365
        5,
                                                                                                                                                                                                                                                                                                                                                                                   2000US-00730E17
2002US-00730E17
2002US-0074978
2002US-035960BP
2002US-035960BP
2002US-035960P
2002US-037860BP
2002US-037860P
2002US-039860P
2002US-039860P
2002US-039860P
                                                                                                                                                                                                                                                                       therapy; vaccine; human
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                                                                                                                                            (first entry)
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        Conservative
                             1 ADCNGAC-----
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J, Taupier RJ;
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SHENOY S G.
SHIMKETS R A.
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CASMAN S J.
GORMAN L.
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                                                                                                                                                                 Human NOV1b protein.
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TAUPIER R J.
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N-PSDB; ADO50841.
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                                                                                                                                                                                                                                                                                            Homo sapiens
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01-MAY-2002;
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         19;
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                                                                                                                       ADO50842;
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(STON/)
(TAUP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BURG/)
(CASM/)
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Best Loc
Matches
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                                                                                RESULT 19
                                                                                         ADO50842
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DB 8; Length 365;

28.2%; Score 62.5;

Sequence 365 AA;

Query Match

L, Ji W, Kekuda R; Shenoy SG, Shimkets RA;

Li L, Padigaru M, Patturajan M, Pena CEA, Stone DJ, Taupier RJ;

WPI; 2003-748127/70

N-PSDB; ADF44662

New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

Claim 1; SEQ ID NO 10; 234pp; English.

asthma, or infections.

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The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, infections, haemophilia, graft-versue-host disease, AIDS (acquired immune deficiency syndrome), asthma, Crohn's disease, miltiple sclerosis, ancexia, cancer-associated cachexia, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, haematopoietic disorders, dyslipidaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridiation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelmithic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; vulner antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexis, cardiovascular disease; infectious disease; anorexis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; haematopoletic disorder; inflammatory skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ADCNGAC-----GFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.2%; Score 62.5; DB 8; Length 365; 33.9%; Pred. No. 38; ive 2; Mismatches 16; Indels 19;
in chromosome mapping, tissue typing or pharmacogenomics.
                                                                            ID NO 4; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF44663 standard; protein; 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV1e protein SEQ ID NO:10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003066881-A2
                                                                    Claim 1; SEQ
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ADF44663
ID ADF44
XX
AC ADF44
XX
AC ADF44
XX
DT 12-FE
DE Human
XX
Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
8
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The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where not is an integer between 1 and 34); (b) a mature form of (a); or (c) a conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:2(n.). (I) and (II) have antidiabetic, anorectic, antidiabetic, antidiabetic, antidiabetic, anotoprotective, antidiatematory, dermatological, and antibodies antidiametory, and antidonvulsant, and antibodies that immunospecifically bind (I), can be used in gene therapy. The polypeptides (I), nucleic acid molecules can metabolic aneuroprotects, and protecting a syndrome associated with a manufacture of a medicament for treating a syndrome associated with a chuman disease. They are useful for treating, preventing or diagnosing (viral, bacterial, fungal, helminthic, and protecoal), anorexia, cancer, cardiovascular diseases (Hypertension, atherosclerosis), cardiovascular diseases (Appertension, atherosclerosis), anorexia, cancer, cardiovascular diseases (Appertension, atherosclerosis), anorexia, cancer, epplepsy, immune disorders, asthma, and various dyslipidaemiae. (I) and antianmacory skin disorders, asthma, and various dyslipidaemiae. (II) and antiangles of the identification of small

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVX; diagnosis; NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension; scleroderma; obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS; acquired immune deficiency syndrome; asthma; Crohn's disease; multiple sclerosis; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.2%; Score 62.5; DB 7; Length 373; 33.9%; Pred. No. 39; ive 2; Mismatches 16; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ADCNGAC------SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
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Best Local Similarity 33.9
Matches 19; Conservative
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08-FEB-2002; 2002US-0355099P. 12-FEB-2002; 2002US-00074978. 12-FEB-2002; 2002US-0356424P. 19-FEB-2002; 2002US-0357928P. 21-FEB-2002; 2002US-03598608P. 27-FEB-2002; 2002US-0359860P.

03-FEB-2003; 2003WO-US003403

14-AUG-2003.

2002US-0375579P.

25-APR-2002; 01-MAY-2002;

17-MAY-2002; 07-JUN-2002; 07-AUG-2002;

2002US-0397002P. 2002US-0393265P. 2002US-0401825P. 2002US-00138588 2002US-0381666P

(CURA-) CURAGEN CORP.

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The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiomyopathy, atherosclerosis, hypertension, scleroma, obesity, cancer, diabetes, infections, haemophila, graft-versus-host disease, ADDS (acquired immune deficiency syndrome), asthma, Crohn's disease, multiple sclerosis, anorexia, cancer-associated cachexia, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, haematopoletic disorders dysliphdaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridisation probes, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes, atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and in chromosome mapping, tissue typing or pharmacogenomics.
haematopoietic disorder; dyslipidaemia; wasting disorder;
chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
gene therapy; vaccine; human.
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Shimkets RA;
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Patturajan M, Pena СЕА, Shenoy SG,
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                                                                                                                                                                             2000US-00730617.
2002US-0355099P.
2002US-00074978.
2002US-0357928P.
2002US-0358608P.
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2002US-00138588.

2002US-0381666P.

2002US-0387002P.

2002US-0393265P.
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                                                                                                                                      16-JUL-2003; 2003US-00357820
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SHENOY S G.
SHIMKETS R A.
STONE D J.
TAUPIER R J.
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PATTURAJAN M.
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GORMAN L.
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BURGESS C I
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                                                                                 JS2004029140-A1
                                                                                                                                                                                                                    19-FEB-2002; 2
21-FEB-2002; 2
27-FEB-2002; 2
24-APR-2002; 2
17-MAY-2002; 2
07-JUN-2002; 2
                                                                                                                                                                               05-DEC-2000; 2
08-FEB-2002; 2
12-FEB-2002; 2
                                                                                                                                                                                                                                                                                                                    02-JUL-2002;
                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stone DJ,
                                                                                                                                                                                                                                                                                                                                              (ANDE/)
(BURG/)
(CASM/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIM/)
(STON/)
(TAUP/)
                                                                                                                                                                                                                                                                                                                                                                                                                (KEKU/)
(LILL/)
(PADI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PENA/)
(SHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PATT/)
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The present invention describes an isolated polypeptide (I) comprising:
    (a) any of the 34 fully defined sequences (P) (see SEQ ID NO:Zn, where n is an integer between 1 and 34); (B) a mature form of (a); or (c) a sequence that is at least 95% identical to (P), or having one or more conservative amino acid substitutions in. (I) can be encoded by a nucleic acid molecule (II), where the sequence is selected from the group consisting of SEQ ID NO:Z(n-1). (I) and (II) have antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, antihelminthic,
                                                                                                                                                                                                                                                                                                                    vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kekuda R;
Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                 185 AECPGGCRNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPG 240
                                                                                                                                                                                                                                                                antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelminthic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiinflammatory; dermatological; antiasthmatic; antilipaemic; antiinflammatory; dermatological; antiasthmatic; unitangingemic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atheroeclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder; asthma; dyslipidaemia.
----SPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w, K
SG, K
                                                                                                                                                                                                                                                     human; antidiabetic; anorectic; cardiant; hypotensive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SJ, Gorman L, Ji
Pena CEA, Shenoy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 12; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /, Burgess CE, Савшап
garu M, Patturajan M,
                                                                                                                                                                                                                    Human NOV1f protein SEQ ID NO:12.
                                                                                                                   ADF44665 standard; protein; 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-0375579P.

2002US-00138588.

2002US-0381666P.

2002US-0387002P.

2002US-0393265P.
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2002US-00074978.
2002US-0356424P.
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2002US-0358608P.
2002US-0359860P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-2003; 2003WO-US003403
                                                                                                                                                                                     12-FEB-2004 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stone DJ, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma, or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-748127/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Padigaru M,
 1 ADCNGAC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003066881-A2.
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27-FEB-2002;
25-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2002;
12-FEB-2002;
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02-JUL-2002;
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                                                                                                                                                    ADF44665;
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                                                                                   RESULT 22
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Gaps

19;

DB 8; Length 373; 16; Indels

28.2%; Score 62.5; D 33.9%; Pred. No. 39; ive 2; Mismatches

Conservative

Query Match Best Local Similarity Matches 19; Conserv

in the

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osteopathic, autivativentry, autivativentry, dermatological, antiasthmatic, antilipaemic, unlinflammatory, dermatological, antiasthmatic, antilipaemic, valinerary and antianglogenic activities, and can be used in gene therapy. The polypeptides (1), nucleic acid molecules (1) and antibodies that immunospecifically bind (1), can be used in the manufacture of a medicament for treating a syndrome associated with a human disease. They are useful for treating, preventing or diagnosing diseases. They are useful for treating, preventing or diagnosing (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), cultimatory skin disorders, asthma, and various dyslipidaemias. (1) and cinflammatory skin disorders, asthma, and various dyslipidaemias. (1) and cinflammatory skin disorders, asthma, and various dyslipidaemias. (1) and differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in gene ration of antibodies that bind immunospecifically to (1) for use in therapeutic or diagnostic methods. (1) can also be used as hybridisation probes, in chromosome mapping, in charantiva madidians and harmanonenemics. The present
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ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue typing, preventive medicine, and pharmacogenomics. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ADCNGAC-----GFCIHPTG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Indels 19;
   nootropic, neuroprotective, antiparkinsonian, anticonvulsant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
28.2%; Score 62.5; DB 7; Length 375;
Best Local Similarity 33.9%; Pred. No. 39;
Matches 19; Conservative 2; Mismatches 16; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 375 AA;
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859999999999999999999858
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atherosclerosis; hypertension; scleroderma, obesity; cancer; diabetes; infection; haemophilia; graft-versus-host disease; AIDS; acquired immune deficiency syndrome; asthma; Crohn's disease; multiple sclerosis; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; haematopoietic disorder; dyslipidaemia; wasting disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic;
                                                                                            diagnosis; NOVX-associated disorder; cardiomyopathy;
ADO50850 standard; protein; 375 AA.
                                                                                                                                                                                             gene therapy; vaccine; human,
                                            15-JUL-2004 (first entry)
                                                                    Human NOV1f protein.
                                                                                                                                                                                                                                           JS2004029140-A1.
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                 12-FEB-2004.
                      ADO50850;
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The present invention relates to novel NOVX polypeptides and their encoding polynucleotides. The invention is useful in diagnosing, treating and preventing NOVX-associated disorders such as cardiomyopathy.

atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes, infections, haemophilia, graft-versus-host disease, AIDS (acquired immune deficiency syndrome), asthma, Crohn's disease, multiple sclerosis, anorexia, cancer-associated cachexia, neurodegenerative disorders such as Alzheimer's disease, parkinson's disease, haematopoietic disorders dyslipidaemias and other wasting disorders associated with chronic diseases. The invention is also useful as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The invention is also useful in gene therapy and in the preparation of vaccines. The present sequence is human NoVX protein.

New NOVX polypeptide, for preventing or treating e.g. cancer, diabetes, atherosclerosis, asthma or acquired immunodeficiency syndrome (AIDS), and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; SEQ ID NO 12; 119pp; English.

Kekuda R; Shimketa RA;

Casman SJ, Gorman L, Ji W, ijan M, Pena CEA, Shenoy SG,

Anderson DW, Burgess CE, Casman

PENA C E A. SHENOY S G. SHIMKETS R A.

STONE D J. TAUPIER R ,

(TAUP/)

SHIM/

STON/ (SHEN/ PENA/

PADIGARU M. PATTURAJAN M.

(LILL/ (PADI/

PATT/

KEKUDA R.

KEKU/

D W

ANDERSON D W. BURGESS C E. CASMAN S J. GORMAN L.

(CASM/) (GORM/) (JIWW/)

Padigaru M, Pad J, Taupier RJ;

Li L, Padi Stone DJ,

WPI; 2004-179665/17.

N-PSDB; ADO50849

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16; Indels 19; Gaps

DB 8; Length 375;

28.2%; Score 62.5; D 33.9%; Pred. No. 39; ive 2; Mismatches

19; Conservative

Best Local Similarity

Matches

Query Match

Sequence 375 AA;

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antinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; neurotropic; neteopathmatic; antiathratic; antirheumatic; antiathratic; antiathratic; antiathratic; antiathratic; antiathratic; antiathratic; antiathratic; thrombolytic; immunomodulator; enterocolitis; zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's Als; neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogenesis; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
                              1 ADCNGAC------GPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                                                                                                                                              ADC78324 standard; protein; 377 AA
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                    Human PRO217 protein.
                                                                                                                                                                                                                             01-JAN-2004
                                                                                                                                                                                     ADC78324;
                                                                                                       RESULT 24
                                                                                                                          ADC78324
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05-DEC-2000; 2000US-00730617. 08-FEB-2002; 2002US-0055099P. 12-FEB-2002; 2002US-00074978. 19-FEB-2002; 2002US-0359608P. 27-FEB-2002; 2002US-0359608P. 25-AFR-2002; 2002US-035960P.

2002US-0381666P 2002US-00138588 2002US-0387002P 2002US-0393265P

01-MAY-2002; 07-JUN-2002;

16-JUL-2003; 2003US-00357820

04-OCT-2000;

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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, Als, neuropathies, dermal scarzing and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple infertility, premature agging, ALDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                       encoding secreted and transmembrane polypeptides with
atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
diabetes; stroke; gene therapy; transgenic; PRO; human.
                                                                                                                                                                                                                                                    Wood WI;
                                                                                                                                                                                                                                                                                                                                                                         homology, e.g. to growth and cancer-associated antigens
                                                                                                                                                                                                                                                    Gurney AL, Hillan K, Pennica D,
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO 4; 355pp; English.
                                                                                                                                                  99WO-US021090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO protein of the invention
                                                                                                                                                                                 98WO-US019330
                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                    Goddard A,
                                                                                                                                                                                                                                                                                                   WPI; 2000-271434/23.
                                                                                                                                                                                                                                                                                                                                                       nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 377 AA;
                                                                                                                                                                                                                                                                                                                    N-PSDB; ADC78323
                                                                                 WO200015796-A2
                                                                                                                                                                                 16-SEP-1998;
                                                                                                                                                  15-SEP-1999;
                                                Homo sapiens
                                                                                                                 23-MAR-2000.
                                                                                                                                                                                                                                                  Chen J,
Yuan J;
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                                                           Gaps
                                             1 ADCNGAC-----GPFEVPPCRSRDC--RCVPIGLFV--GFCIHPTG 37
                         19;
  DB 3; Length 377;
                       16; Indels
28.2%; Score 62.5; Di
33.9%; Pred. No. 39;
iive 2; Mismatches
         Local Similarity 33.9
  Query Match
                       Matches
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human; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; virucide; antibacterial; fungicide; protozoacide; antihelminthic; nootropic; neuroprotective; antihelminthic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antinflammatory; dermatological; antiasthmatic; antilipaemic; vulnerary; antiangiogenic; gene therapy; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cardiovascular disease; hypertension; atherosclerosis; neurodegenerative disorder; Alzhelmer's disease; Parkinson's disease; epilepsy; immune disorder; osteoarthritis; haematopoietic disorder; inflammatory skin disorder;
                                          ADF44671 standard, protein, 377 AA
                                                                                                                                                              Human NOV11 protein SEQ ID NO:18.
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             asthma; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                        12-FEB-2004
                                                                                  ADF44671;
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Gaps

19;

16; Indels

DB 7; Length 377;

ch 28.2%; Score 62.5; DE Similarity 33.9%; Pred. No. 39; 19; Conservative 2; Mismatches

Best Local Similarity

Matches

Query Match

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The present invention describes an isolated polypeptide (I) comprising:

(a) any of the 34 fully defined sequences (P) (see SEQ ID NO:2n, where not is an integer between 1 and 34); (b) a mature form of (a); or (c) a conservative between 1 and 34); (b) a mature form of (a); or (c) a conservative amino acid substitutions in. (I) can be encoded by a mucleic consisting of SEQ ID NO:2(n-1). (I) and (II) have antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, or virucide, antibacterial, fungicide, protozoacide, antihelminthic, corecopathic, antiarthritic, antiarthriammatory, dermatological, antiarthritic, antiarthritic, antiarthriammatory, dermatological, antiarthritic, antiarthriammatory, dermatological, antiarthritic, antiarthriammatory, dermatological, and antibodies that immunospecifically bind (I), can be used in the manufacture of a medicament for treating a syndrome associated with a human disease. They are useful for treating preventing or diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, sethemses, obesity, infectious disease, consultation, also be used as targets for the identification of small consultation, cell proliferation, hemmatory shuth and various dysliptidemias. (I) and cardiovascular modulate or inhibit e.g. neurogenesis, cell immunospecifically to (I) can also be used as targets for the identification of small or immunospecifically to (I) can be used as hybridiastion probes, in chromosome mapping, immune the propertion of antibodies that prosent in the probes, in the propertice or inhibit or in canding expension or dispensed in the propertice. The propertice of the propertice or inhibit or in the probes in the propertice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kekuda R;
Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preventive medicine, and pharmacogenomics. The present of in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DW, Burgess CE, Casman SJ, Gorman L, Ji W,
Li L, Padigaru M, Patturajan M, Pena CBA, Shenoy SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 18; 234pp; English.
                                                                                                                                                              2002US-00074978
2002US-0356424P
2002US-0358608P
2002US-035860P
2002US-035860P
2002US-0375579P
2002US-00138588
2002US-00138588
                                                                                                                                                                                                                                                                                                                                       07-JUN-2002; 2002US-0387002P.
02-JUL-2002; 2002US-0393265P.
07-AUG-2002; 2002US-0401825P.
                                                                                                      03-FEB-2003; 2003WO-US003403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone DJ, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, or infections
                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-748127/70.
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                    WO2003066881-A2
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                                                            14-AUG-2003
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